

DATA EVALUATION RECORD
HONEYBEES FIELD TEST
Apis mellifera
Non-Guideline Semi-Field Tunnel and Field Trial Residue Study

1. **CHEMICAL**: Sulfoxaflor PC Code No.: 005210
2. **TEST MATERIAL**: GF-2032 (ai: Sulfoxaflor) Purity: 21.8% w/w; 241 g/L

3. **CITATION**

Author: JH Howerton and LM Gilson

Title: GF-2032: Effects and Determination of Residues on Honeybee (*Apis mellifera* L.) Adults and Brood in Semi-Field Test Conditions.

Study Completion Date: June 28, 2018

Laboratory: SynTech Research Inc., Stilwell, Kansas

Sponsor: Dow AgroSciences LLC, Indianapolis, IN

Laboratory Report ID: 014SRFR15C08

DP Barcode: 447927

MRID No.: 50604601

4. **REVIEWED BY**: Moncie V. Wright, Ph.D., CDM/CSS-Dynamac JV

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Date: 10/9/2018

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Date: 10/24/2018

5. **APPROVED BY**: Meghann Niesen, Ecologist, OPP/EFED/ERB5

Signature:

6. STUDY PARAMETERS

Test Species: Honeybees (*Apis mellifera* L.)

Age of Test Organism at Test Initiation: Healthy colonies contained one queen with ~9,000 bees, 3,000 cells with brood, 2 frames with honey, and 0.5 frame of pollen.

Test Duration: 9-day exposure with additional 9 months of monitoring

7. CONCLUSIONS: GF-2032 (ai: Sulfoxaflor) was applied at nominal rates of 0 (negative tap water control), 0.023, 0.071, and 0.089 lb ai/acre to flowering plants (*Fagopyrum esculentum*) in Stilwell, Kansas with two reference controls. The first reference group was treated with Dimethoate at an actual rate of 0.055 lb ai/acre, while the second was treated with Rimon at an actual rate of 0.079 lb ai/acre. The measured application rates of sulfoxaflor were 0.027, 0.065, and 0.083 lb ai/acre.

The honey bee (*Apis mellifera*) colonies were exposed for 9 days using 8 replicate tunnel tents in the control and 6 replicate tunnels in each treatment level. An additional replicate tunnel was established in each control and treatment group for the purpose of residue quantification. Residues were quantified for nectar, pollen, and whole plants. Following the 9-day test exposure, the hives were monitored for an additional 9 months at another site. Mortality, flight activity, colony condition, and bee brood development were assessed.

All endpoints were seemingly affected in this experiment at one or multiple sampling events. Residues were detected in all matrices, and DT₅₀ values calculated when possible.

REVIEWER'S CONSIDERATION OF STUDY STRENGTHS, LIMITATIONS, AND INTERPRETATION

It is important to recognize the inherent strengths and limitations of this study as results are interpreted and potentially considered in risk assessment.

In the context of available field studies involving honey bees, this study contains some strengths including:

- Inclusion of multiple colony-level endpoints reflecting hive condition, brood development, and nectar/pollen availability.
- Availability of raw data for conducting statistical analysis.
- Quantification of exposure to sulfoxaflor in the application solutions used to treat the crops.
- DT₅₀ values were estimated for the parent material in all matrices at each treatment level.

A number of limitations were noted, including:

- Samples for the residue portion were only collected for 7 days after application. As a consequence, the residue data represent a short observation period and were present at low levels at the end of 7 days.
- Storage and transit stability of the residue samples collected were not determined.
- Overwintering survival was very poor in control hives which excludes use of that endpoint in analysis.

8. ADEQUACY OF THE STUDY: This study is scientifically sound and is classified as supplemental (quantitative).

9. GUIDELINE DEVIATIONS: This semi-field study was conducted following the OECD guidance document No. 75 (2007) and OEEP/EPPO Guideline No. 170 (2010).

10. SUBMISSION PURPOSE: This study was conducted to investigate the potential effects of **GF-2032 (ai: Sulfoxaflor)** exposure to honey bee (*Apis mellifera*) mortality, flight activity, brood development, colony condition, and residues after application to flowering plants (*Fagopyrum esculentum*).

11. MATERIALS AND METHODS

Test Material:

Identity:	GF-2032 (ai: Sulfoxaflor)
IUPAC name (ai):	not reported
CAS name (ai):	N-[methyloxido[1-[6-(trifluoromethyl)-3-pyridinyl]ethyl]- λ4-sulfanylidene]cyanamide
CAS No.:	946578-00-3
Lot No.:	D523G2A003
Description:	Tan liquid
Purity:	21.8% w/w (241 g/L)
Storage:	+5°C to +30°C (Actual temperature range: 15.5 – 24.0 °C)

Test Organisms/Hives: The honeybees (*Apis mellifera* L.) used in the test were obtained from colonies that were purchased from Heartland Honey, Spring Hill, Kansas. While target criteria were set for each colony and attempts were made to attain proper colony size and resources, there were colonies that either exceeded or did not meet some of the criteria. The study author determined that the colonies were acceptable for the study conditions. The colonies had all brood development stages present and all queens were <1 year old. Colonies were not treated with medication or chemicals in the four weeks prior to test initiation.

The test colonies were housed in Langstroth hive bodies with newly purchased hive frames. Prior to study initiation, the colonies were visually inspected to be disease free. Varroa mite and Nosema spore levels were assessed.

Test Design: The semi-field test location was located in Stilwell, Kansas in a full flowering buckwheat (*Fagopyrum esculentum*) field. The field site was divided into 6 plots (one control, three treatment groups, and two reference groups). The control had 9 replicates (tunnels), the treatments had 7 replicates, and the reference groups had 3 replicates. Of the replicates established for each group, one replicate was allocated solely to residue sample collection of bee matrices. Each tunnel tent covered 2500 ft² (125 ft length x 20 ft width x 10 ft height) and was covered with mesh netting (4-5 mm). The distance between the control and treated tunnels was ~50 ft. During the tunnel exposure period, the bees were supplied with water in buckets that contained sponges to prevent the honey bees from drowning. The bees were released into the tunnels at 3 days prior to application of the test material.

During the tunnel phase, bees could freely forage on buckwheat. The adjacent flowering crops that were unavailable included, corn, sugar beet, soybean, sorghum, pepper, buckwheat, and clover. Buckwheat was planted at the isolation site as a source of nectar for the bees. Ornamental flowers were within range of the colonies at that site. After the exposure phase, the bees were transported to an isolation site and were monitored and cared for according to standard beekeeping practices.

Application rates: The nominal actual application rates were 0 (negative tap water control), 0.023, 0.071, and 0.089 lb ai/acre. The first reference group was treated with Dimethoate at an actual rate of 0.055 lb ai/acre, while the second was treated with Rimon at an actual rate of 0.079 lb ai/acre. The measured application rates of the test material were 0.027, 0.065, and 0.083 lb ai/acre.

Application procedure: The treated spray solutions were prepared shortly before the application and applied using a backpack boom sprayer with Tee Jet flat fan nozzles (8002VS) and an operating pressure of 20 psi. during bee flight to ensure contact exposure occurred. Thorough mixing of the solutions was performed to obtain homogeneity of the solutions. The equipment used to apply spray solutions was calibrated within 24 hours prior to use. Samples were collected from the stock solution mixing tanks and from spray boom nozzles prior to and after application. During all applications, wind speed did not exceed 2.7 mph, air temperature was 83.2-92.3°F, and humidity was 61.1-76.7%.

The hive bodies were covered with cardboard during application to prevent contamination of the hive exterior, while permitting foraging bees to enter and leave the hive. The water buckets were also removed during application to prevent contamination.

After application the covers were removed, and the buckets replaced.

Methods: Brood cells from 8 frame sides in the colonies were photographed prior to application of the test material. Honeybee Complete Software (WSC Scientific GmbH, Heidelberg, Germany) was used to record and track brood status in individual cells. The brood cells (eggs, larvae, pupae, and capped brood) were assessed for mortality by frame side in each colony for two brood cycles. All distinguishable eggs and larva cells were identified and recorded by an assessor. The first brood cycle was assessed at -2, 4, 8, 15, and 19 days after application (DAA), which corresponded to BFD, BFD+6, BFD+10, BFD+17, and BFD+21, respectively. The second brood cycle was evaluated with a new set of brood at 19, 26, 31, 36, and 43 DAA.

Brood termination rate (failure of brood development based on cell content of eggs, larvae, or pupae) was quantified using Honeybee Complete, which calculated the rate based on the number of cells where termination of bee brood development was recorded by the assessor versus the number of initially marked eggs.

Brood index (an indicator of bee brood development) was calculated for each assessment day. Cells were rated from 1 to 5 if they contained the expected brood stage, but if they did not, then the cell was rated a 0 at that assessment day and every day thereafter regardless if the cell again filled with brood. For the final calculation, the values of all individual cells in each group assessed at the same date were summed and divided by the total number of observed cells.

The brood compensation index (an indicator for colony recovery) was assessed similarly to brood index. Cells were classified from a rating of 1 to 5 based on the identified growth stage on the respective assessment day. If there was no brood in a cell and the cell was filled with pollen or nectar, the cell was rated a 0. For the final calculation, the values of all individual cells in each group assessed at the same date were summed and divided by the total number of observed cells.

Colony health assessments were performed by visual inspection of each hive. Abnormal behavior, disease, and the presence of a queen, eggs, and/or queen cells were recorded. Quantitative estimates were made for the percentage of bee coverage, empty space, nectar/honey, pollen, capped brood, and open brood. The total bee hive population was estimated by multiplying the mean % coverage for all frames by the maximum coverage of bees possible on a frame side by the total number of frames. The number of cells containing honey/nectar, pollen, capped brood, or open brood was calculated using an equation that considered the total % frame side coverage and the total number of cells occupying one frame side.

Mortality was determined based on dead bees (adults, larvae, and pupae) observed in bee

traps and on sheets lining the ground in the tunnels. At the time of the assessment, dead bees and debris were removed from the traps and sheets.

Foraging bees and bees in flight were counted over a 15 second interval inside three marked areas in each tunnel (measured 1 x 1 m). Photographs were taken to try to determine variation of crop coverage from tunnel to tunnel. The number of flowers in the photos were counted.

Samples of pollen from pollen traps, forager bees, and whole plants were collected over seven sampling events during full bloom (-1, 0, 1, 2, 3, 4, and 7 DAA). All samples were stored in coolers with dry ice until transfer to permanent frozen storage. Analysis and retain samples were collected when possible. Forager bees were collected in jars in the field. Pollen loads from forager bees were collected using pollen traps set up on the hives the evening before each sampling event. The traps were emptied by the end of bee flight each sampling day, and pollen was transferred to amber glass vials using forceps. Forager bees were collected as they returned to the hive using nets, then the bees were transferred to jars containing dry ice and stored frozen until honey stomach processing could be completed. Honey stomachs were removed in the laboratory and stored in autosampler vials (2-ml), which were then placed into an amber glass vial. Whole plants were sampled from at least 12 areas of the plot by pulling them from the ground, and attached roots were removed before double-bagging the plant samples.

Residue Analysis Method: All residue analyses were conducted at SynTech Research Laboratory Services, LLC (SRLS) in Stilwell, Kansas. The LOQ for sulfoxaflor and its metabolites was identified by the study sponsor to be 0.010 mg/kg in pollen and whole plant, and 0.001 mg/kg in nectar. The LOD was identified by the sponsor to be 0.003 mg/kg in pollen and whole plant, and 0.0003 mg/kg in nectar.

The method was successfully verified for nectar, pollen, and whole plants, and the mean recoveries were 70-137% for nectar and pollen and 89-98% for whole plants. Samples were analyzed using LC-MS/MS.

Statistical Analysis: Data were analyzed using CETIS statistical software v.1.8.7.4. All data were organized and analyzed for each timepoint of collection and each replicate, with the exception of mortality data where timepoints were summed to provide pre- and post-application total mortality data. There were insufficient data for larval mortality so the analyses were inconclusive and not included in the MRID.

All data were considered continuous data and were transformed using the Log (Y+Z) transformation for continuous data prior to analysis. Angular transformations were used on proportional data. Any zero values that were problematic had 0.01 added to the zero values so analyses could be conducted. All analyses were conducted using one-tailed

tests for events following application of the test material. Analyses of data collected prior to application were conducted using two-tailed tests.

Data of the treatment groups and the control were checked for normality and homogeneity of variance. Parametric data were analyzed using Dunnett's test and nonparametric data were analyzed using the Dunn-Bonferroni/Holm test. In some cases, different methods were used depending on data monotonicity.

Summary of Study Dates:

Targeted Study Day	Actual Date	Event
NA	5/5/16 (-38 DAA)	Crop planted
NA	6/7/16 (-5 DAA)	Tunnels completed
NA	6/9/16 (-3 DAA)	Honey bees released in tunnels
-2 DAA	6/10/16 and 6/11/16 (-2 DAA and -1 DAA)	BFD 1 – initial photographs of all frames in each colony
0 DAA	6/12/16 (0 DAA)	Foliar application of GF-2032
3 DAA (± 1)	6/16/16 (4 DAA)	Brood development
8 DAA (± 1)	6/20/16 (8 DAA)	Brood development / colony assessment
10 DAA (± 1)	6/22/16 (10 DAA)	Hives moved to isolation site
14 DAA (± 1)	6/27/16 (15 DAA)	Brood development
20 DAA (± 1)	7/1/16 (19 DAA)	BFD 2 - Brood development
26 DAA (± 1)	7/8/16 (26 DAA)	Brood development / colony assessment
31 DAA (± 1)	7/13/16 (31 DAA)	Brood development
36 DAA (± 1)	7/18/16 (36 DAA)	Brood development
42 DAA (± 1)	7/25/16 (43 DAA)	Brood development / colony assessment
BFD to 54 DAA	6/10/16 – 8/4/16 (BFD to 54 DAA ¹)	Mortality of adults, larvae, and pupae in traps assessed
BFD to 10 DAA	6/10/16 – 6/21/16 (BFD to 9 DAA ¹)	Mortality of adults, larvae, and pupae in tunnels assessed
BFD to 10 DAA	6/10/16 – 6/21/16 (BFD to 9 DAA ¹)	Flight activity assessed daily
Fall Assessment	9/12/16 – 9/22/16	Colony Assessment
NA	10/25/16	Crop destruct
Spring Assessment	3/28/17	Colony Assessment

¹Hives were transported to the isolation site on the morning of 10 DAA. No mortality or flight activity data was collected that day. See Deviation 4.

12. REVIEWERS RESULTS

Statistics. For the reviewer calculated results statistics were run using R programing (R Core Team 2013). As the data permitted comparisons were run between control and treatment groups as outlined in Appendix A. Where appropriate Dunnett's test or Wilcoxon tests were

used for these comparisons.

Adult Mortality. Adult foraging bees exposed to GF-2032 at rates of 0.090, 0.071, and 0.023 lb a.i./A (during flight) exhibited a statistically-significant increases in mortality of up to 20X the rate observed in controls on the day of application. This increase in mean daily worker bee mortality was short lived, however, having returned to not significantly different from controls by 2DAA (for the 0.023 lb a.i./A treatments) and 3DAA (for the 0.071 and 0.090 lb a.i./A treatment). Significant spikes in mortality were seen in the 0.071 treatment level until the end of observation 9DAA.

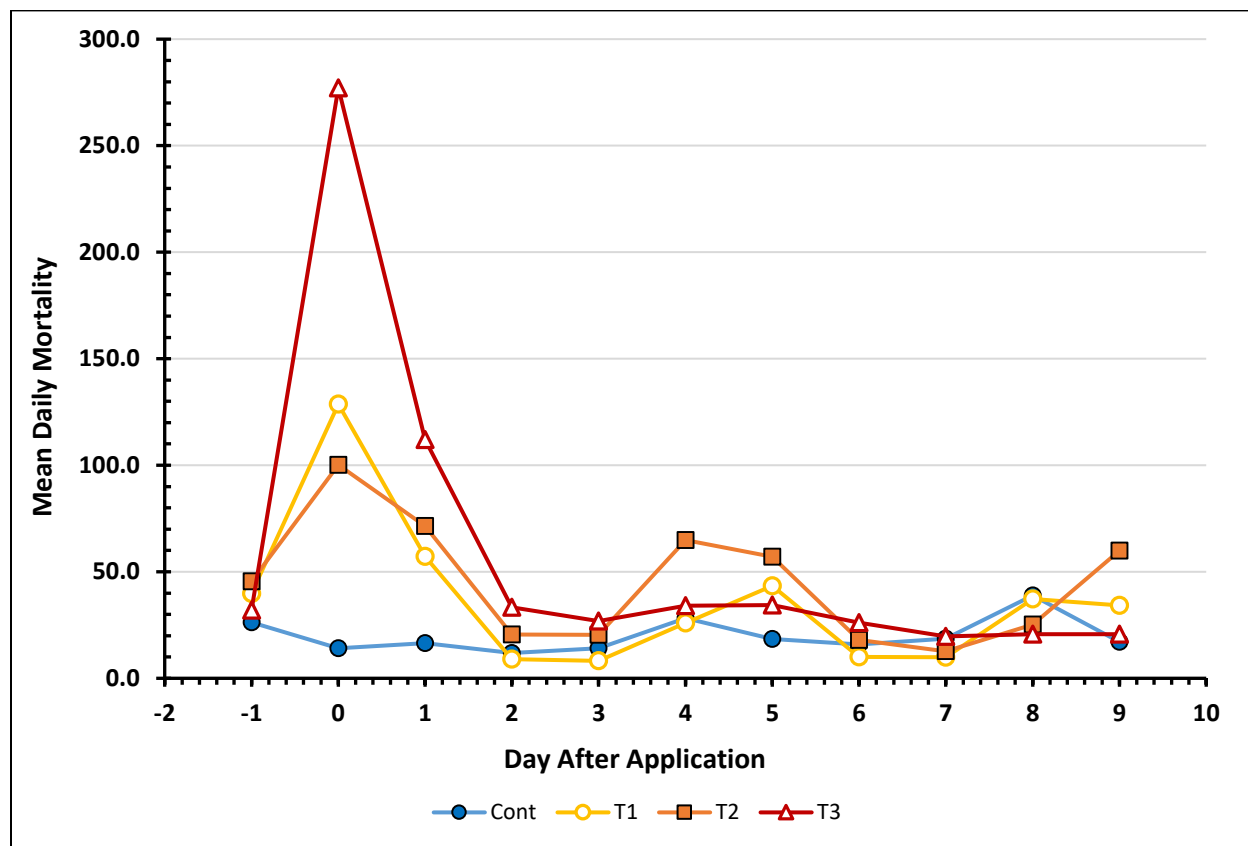


Figure 1. Mean number of dead adult bees per day.

Foraging Activity. There were significant decreases in flight intensity in the treatment groups as compared to the control during the entire exposure period. This endpoint was highly variable within the same group over time, fluctuating up and down in a manner likely attributable to chance.

Colony Strength. The effect of sulfoxaflor on colony strength is difficult to interpret due to

large variation between hives. There were no sustained effects to colony strength at any timepoint. There were no obvious dose-dependent trends in colony strength apparent among hives. Honey stores were significantly different from control at 43DAA. Number of brood was significantly different from controls for the 0.023 treatment level at 26DAA, for the 0.071 treatment level in the Fall, and for the 0.090 treatment level at 8DAA. These differences were not sustained between these timepoints or constant between treatment levels.

Brood Condition. The brood and compensation indices for eggs were reduced in the highest application group in the first brood cycle. The brood and compensation indices for young larvae were reduced in the lowest and highest application group in the first brood cycle. The brood and compensation indices for old larvae were reduced in the lowest application group in the first brood cycle. The termination rate for eggs, young larvae, and old larvae was increased in all treated groups in the first brood cycle.

The brood index, compensation index, and termination rate for eggs, young larvae, and old larvae appeared unaffected by treatment in the second brood cycle. The termination rate for eggs in the second brood cycle was notably reduced in the highest application group as compared to the control.

Residues. Residues of sulfoxaflor up to 2.37 mg/kg were detected in bee collected nectar in the 0.09 lb a.i./A treatment group and showed decline over time after the peak at 2DAA. Residues in nectar were less in the 0.071 and 0.023 treatment groups but followed the same decline trend. Residues of sulfoxaflor in bee collected pollen up to 2.48 mg/kg were detected in the 0.09 lb a.i./A treatment group and declined over time after the peak at 2DAA. In both pollen and nectar 7 days was not enough for residues to drop below the limit of detection for sulfoxaflor.

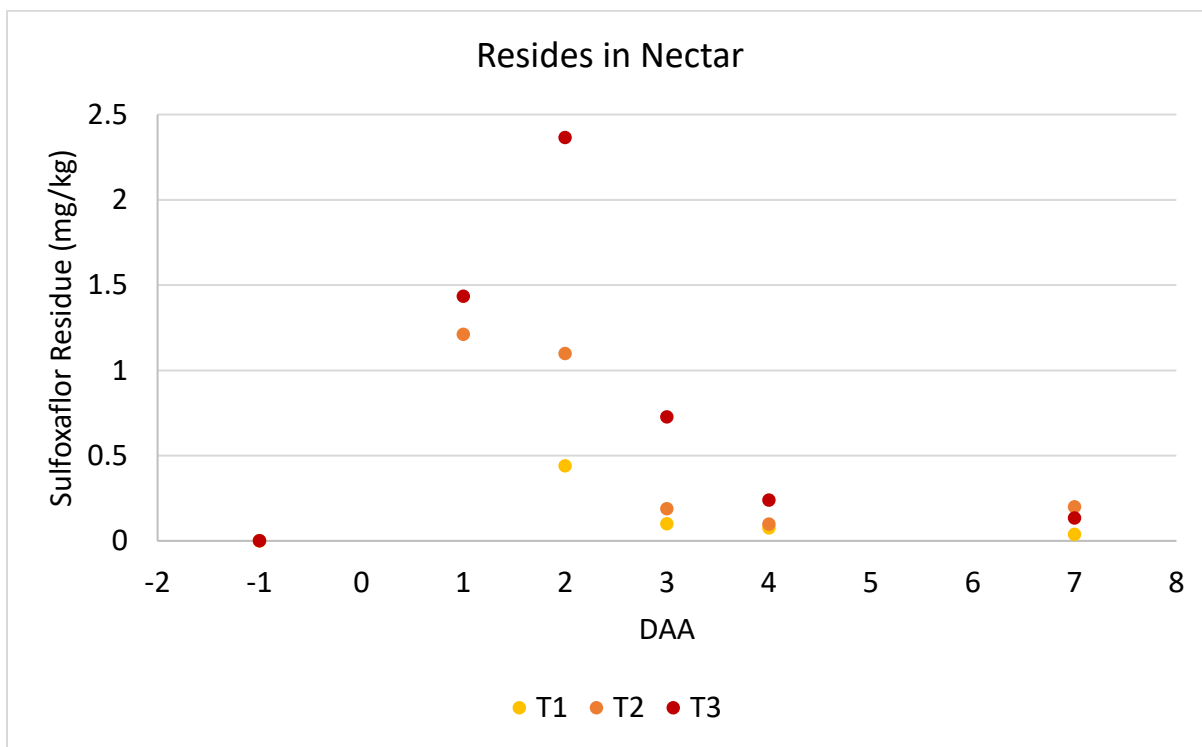


Figure 2. Sulfoxaflor residues from bee collected nectar per day after application.

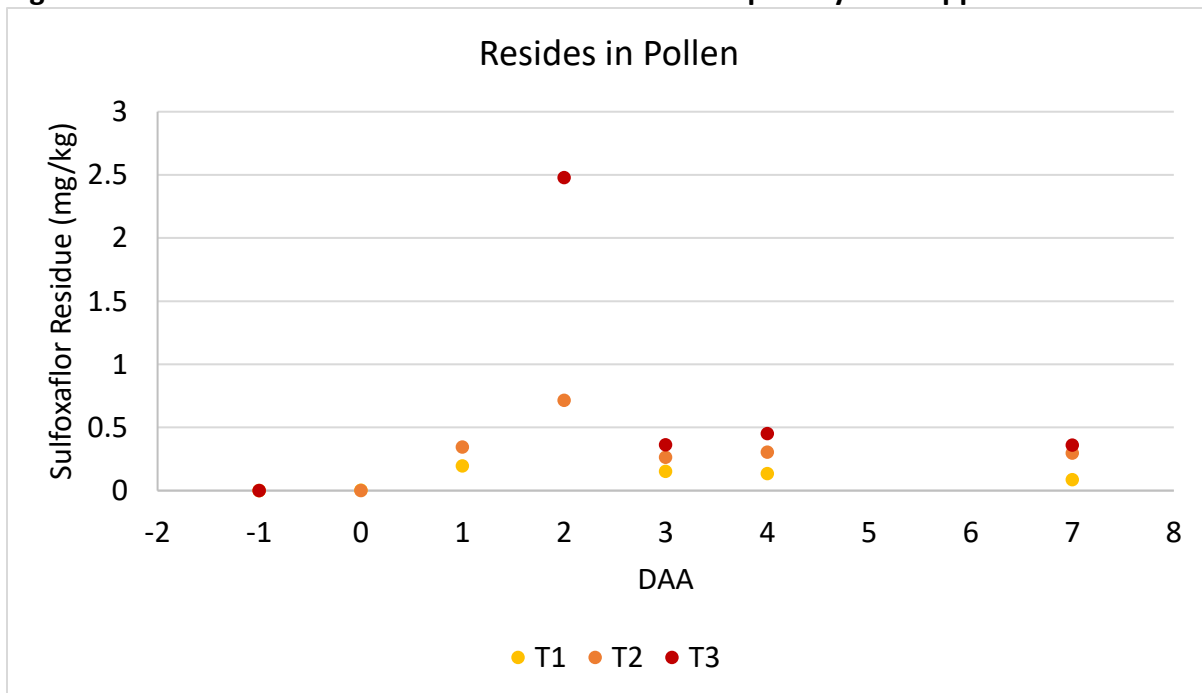


Figure 3. Sulfoxaflor residues from bee collected per day after application.

Overwintering. The majority of colonies were lost in the late winter. With 63% mortality in the controls; 67% mortality in T1; 83% mortality in T2 and 50% mortality in T3. High control mortality confounds the interpretation of impact of sulfoxaflor treatment on overwintering success.

DT₅₀. In this study, separate trials (tunnels) were evaluated with three different foliar spray application rates during bloom (0.023, 0.071, and 0.089 lb a.i./A). Since only one composite replicate was collected during each sampling event, the individual trial data are considered insufficient for reliable DT₅₀ calculation due to lack of variability within a sampling event. Therefore, these data were normalized to the peak concentration within each trial and combined for DT₅₀ determination. Among both matrices, DT₅₀ values varied from 1.2 days (nectar) to 2.7 days (pollen), indicating relatively rapid decline of sulfoxaflor in bee-relevant matrices. These DT₅₀ values indicate that repeated application of sulfoxaflor would not lead to additional accumulation in pollen and nectar (*e.g.*, no or negligible carry over) with the proposed minimum 7-d retreatment interval. Output from the modeling used to calculate these values is in Appendix B.

Table 1. DT₅₀ and DT₉₀ values for sulfoxaflor in buckwheat matrices

Crop (Region)	DT ₅₀ Values	DT ₉₀ Values
Nectar from Bees		
Buckwheat (Kansas)	1.2	4.0
Pollen from Traps		
Buckwheat (Kansas)	2.7	8.8

13. STUDY AUTHOR REPORTED RESULTS

Mortality: At -1DAA, mortality was similar between the controls and groups exposed to the test material. At 0DAA (post-application), mortality was increased by an order of magnitude in all treatment groups as compared to the control. This persisted in only the highest application group at 1DAA, with increases noted in the other two application groups. By 2DAA, mortality was only slightly increased in the two highest application groups. At 9DAA, mortality was comparable between the controls and three application groups when accounting for the high variability in the two lowest application groups.

Table 2. Mean mortality of adult bees in dead bee traps and sheets

Measured Treatment, lb ai/A	Observation Day Interval					
	-1DAA	0DAA post treatment	1DAA	2DAA	6DAA	9DAA
Adult Bees (mean \pm SD)						
Control	26 \pm 14	14 \pm 5	17 \pm 8	12 \pm 3	16 \pm 14	17 \pm 8
0.027	40 \pm 15	129 \pm 27	57 \pm 46	9 \pm 9	10 \pm 8	34 \pm 30
0.065	46 \pm 20	100 \pm 6	72 \pm 32	21 \pm 12	18 \pm 8	60 \pm 38
0.083	32 \pm 14	277 \pm 89	112 \pm 49	33 \pm 16	26 \pm 11	21 \pm 7

DAA=Days After Treatment

Flight Activity: Flight activity (no. of bees/minute) was similar between the control and three groups exposed to the test material. At 0DAA (post-application), flight activity was notably decreased in all three application groups. By 1DAA, flight activity was more similar to the control. From 2DAA to 9DAA, flight activity was suppressed in all three application groups.

Table 3. Flight Activity (no. of honey bees/minute, mean \pm SD)

Measured Treatment, lb ai/A	Observation Day Interval						
	-1DAA	0DAA post	1DAA	2DAA	3DAA	6DAA	9DAA
Control	6 \pm 3	72 \pm 13	36 \pm 6	39 \pm 14	35 \pm 6	32 \pm 11	41 \pm 13
0.027	11 \pm 7	17 \pm 6	28 \pm 8	12 \pm 2	12 \pm 5	9 \pm 4	7 \pm 3
0.065	8 \pm 7	15 \pm 5	24 \pm 12	5 \pm 3	17 \pm 5	15 \pm 3	17 \pm 12
0.083	5 \pm 3	6 \pm 3	13 \pm 10	3 \pm 5	9 \pm 2	13 \pm 6	17 \pm 14

DAA=Days After Treatment

Colony Condition: The total number of adult bees, and cells containing capped and open brood was similar in the control and all three exposure groups at every sampling interval, from -2DAA to the last assessment to overwintering (Fall 2016). For the total number of cells containing honey/nectar, there were reductions in one or both of the two highest application groups at all assessments from -2DAA to 43DAA. Effects had subsided by Fall 2016.

For the total number of cells containing pollen, there were reductions in the lowest application group at all assessments from -2DAA to 43DAA. Effects had subsided by Fall 2016. Results for the first overwintering assessment (Spring 2017) were not reliable due insufficient surviving replicates.

Table 4. Summary of Colony Conditions

Colony Condition Parameter	Measured application rate (lb ai/A)			
	Control	0.027	0.065	0.083
1st Colony Assessment: -2DAA = BFD 1 (mean \pm SD)				
Adult Bees (Total No.)	10377 \pm 2289	9854 \pm 1154	8862 \pm 1136	7921 \pm 1654
Cells containing capped brood (No.)	21553 \pm 1796	21875 \pm 2937	22677 \pm 4437	22050 \pm 4099

Colony Condition Parameter	Measured application rate (lb ai/A)			
	Control	0.027	0.065	0.083
Cells containing open brood (No.)	21057 ± 4599	20935 ± 4321	19158 ± 5026	18671 ± 2768
Cells containing honey/nectar (No.)	10920 ± 3804	12401 ± 3253	8743 ± 4043	7907 ± 5220
Cells containing pollen (No.)	5486 ± 3206	3309 ± 1278	4180 ± 2216	6235 ± 1853
2nd Colony Assessment: 8DAA (mean ± SD)				
Adult Bees (Total No.)	13692 ± 2833	13125 ± 1900	13303 ± 2625	12394 ± 2311
Cells containing capped brood (No.)	17765 ± 4575	13690 ± 3051	17800 ± 4566	11286 ± 2498
Cells containing open brood (No.)	14891 ± 7324	8047 ± 2319	15362 ± 4782	11913 ± 4418
Cells containing honey/nectar (No.)	8334 ± 4029	9962 ± 3351	9823 ± 5046	5991 ± 5734
Cells containing pollen (No.)	1280 ± 1534	2578 ± 2352	418 ± 374	2369 ± 2003
3rd Colony Assessment: 26DAA = BFD2 (mean ± SD)				
Adult Bees (Total No.)	12446 ± 1279	10690 ± 1142	12415 ± 1133	12498 ± 1593
Cells containing capped brood (No.)	16694 ± 7438	17452 ± 1742	14038 ± 9795	17730 ± 8955
Cells containing open brood (No.)	13533 ± 5210	21423 ± 3541	15989 ± 12534	13655 ± 7280
Cells containing honey/nectar (No.)	17216 ± 6147	19542 ± 5653	12993 ± 6657	9928 ± 4209
Cells containing pollen (No.)	5930 ± 3844	4703 ± 1340	3797 ± 1908	5957 ± 2175
4th Colony Assessment: 43DAA (mean ± SD)				
Adult Bees (Total No.)	14554 ± 3402	13031 ± 1655	11255 ± 3147	13460 ± 3902
Cells containing capped brood (No.)	20299 ± 9095	18915 ± 2806	14944 ± 9956	17556 ± 7064
Cells containing open brood (No.)	13585 ± 5872	21214 ± 5763	15536 ± 10535	12122 ± 3527
Cells containing honey/nectar (No.)	20691 ± 6232	17312 ± 7093	8499 ± 5872	6479 ± 4142
Cells containing pollen (No.)	4467 ± 3744	2961 ± 1243	5016 ± 3605	4041 ± 1941
5th Colony Assessment: Fall 2016 (mean ± SD)				
Adult Bees (Total No.)	18971 ± 3315	18047 ± 2020	19801 ± 6997	21782 ± 4940
Cells containing capped brood (No.)	18131 ± 6400	22851 ± 5716	19646 ± 2313	22948 ± 5392
Cells containing open brood (No.)	9853 ± 4597	12227 ± 1859	16302 ± 4773	14463 ± 4783
Cells containing honey/nectar (No.)	38665 ± 9888	44587 ± 11146	33064 ± 18679	38916 ± 14938
Cells containing pollen (No.)	6389 ± 2706	5643 ± 1808	9280 ± 2134	7315 ± 4461

Colony Condition Parameter	Measured application rate (lb ai/A)			
	Control	0.027	0.065	0.083
6th Colony Assessment: Spring 2017 (mean \pm SD)				
Adult Bees (Total No.)	12352 \pm 1466	3574 \pm NA	17995 \pm NA	12394 \pm 11251
Cells containing capped brood (No.)	16093 \pm 1271	627 \pm NA	20691 \pm NA	10171 \pm 9835
Cells containing open brood (No.)	19158 \pm 4767	627 \pm NA	24035 \pm NA	6897 \pm 6985
Cells containing honey/nectar (No.)	28285 \pm 1740	22572 \pm NA	56639 \pm NA	17486 \pm 13529
Cells containing pollen (No.)	7594 \pm 3031	7524 \pm NA	8151 \pm NA	7733 \pm 7189

NA= not applicable, insufficient replicates for calculation

Development of Bee Brood: The brood and compensation indices for eggs were reduced in the highest application group in the first brood cycle. The brood and compensation indices for young larvae were reduced in the lowest and highest application group in the first brood cycle. The brood and compensation indices for old larvae were reduced in the lowest application group in the first brood cycle. The termination rate for eggs, young larvae, and old larvae was increased in all treated groups in the first brood cycle.

The brood index, compensation index, and termination rate for eggs, young larvae, and old larvae appeared unaffected by treatment in the second brood cycle. The termination rate for eggs in the second brood cycle was notably reduced in the highest application group as compared to the control.

Table 5. Brood Index, Compensation Index, and Termination Rates for Eggs, Young Larvae, and Old Larvae

Measured Application Rate, lb ai/A	Observation Interval	
	First Brood Cycle	Second Brood Cycle
Eggs		
Brood index (mean \pm SD)		
Control	2.61 \pm 1.19	4.25 \pm 0.31
0.027	1.85 \pm 0.92	3.86 \pm 0.57
0.065	2.05 \pm 1.23	4.06 \pm 0.35
0.083	1.15 \pm 0.79	4.46 \pm 0.30
Compensation index (mean \pm SD)		
Control	2.89 \pm 1.17	4.43 \pm 0.32
0.027	2.48 \pm 0.81	4.20 \pm 0.42
0.065	2.25 \pm 1.25	4.30 \pm 0.29
0.083	1.59 \pm 1.07	4.62 \pm 0.28
Termination rate (mean \pm SD)		
Control	47.90 \pm 23.90	22.90 \pm 9.71
0.027	63.08 \pm 18.32	26.98 \pm 12.20
0.065	59.01 \pm 24.59	24.93 \pm 6.17
0.083	76.93 \pm 15.89	17.32 \pm 6.54
Young larvae		
Brood index (mean \pm SD)		
Control	3.59 \pm 1.35	4.41 \pm 0.32
0.027	1.53 \pm 1.16	4.68 \pm 0.15
0.065	3.21 \pm 1.15	4.32 \pm 0.34
0.083	1.49 \pm 1.00	4.61 \pm 0.38
Compensation index (mean \pm SD)		
Control	4.07 \pm 0.72	4.60 \pm 0.21
0.027	2.18 \pm 1.03	4.79 \pm 0.10
0.065	3.55 \pm 0.89	4.53 \pm 0.45
0.083	2.31 \pm 1.04	4.71 \pm 0.36
Termination rate (mean \pm SD)		
Control	28.20 \pm 26.90	11.85 \pm 6.49
0.027	69.44 \pm 23.28	6.31 \pm 2.94
0.065	35.81 \pm 23.06	13.68 \pm 6.87
0.083	70.22 \pm 20.05	7.83 \pm 7.62
Old larvae		
Brood index (mean \pm SD)		
Control	4.41 \pm 0.66	4.88 \pm 0.10
0.027	3.29 \pm 0.76	4.95 \pm 0.02
0.065	3.99 \pm 1.12	4.85 \pm 0.12
0.083	4.09 \pm 0.53	4.92 \pm 0.04
Compensation index (mean \pm SD)		
Control	4.62 \pm 0.32	4.93 \pm 0.05
0.027	3.67 \pm 0.66	4.98 \pm 0.01
0.065	4.18 \pm 0.92	4.94 \pm 0.04
0.083	4.35 \pm 0.47	4.95 \pm 0.05
Termination rate (mean \pm SD)		

Control	11.79 ± 13.21	2.40 ± 1.97
0.027	34.23 ± 15.27	1.00 ± 0.46
0.065	20.18 ± 22.32	3.06 ± 2.48
0.083	18.16 ± 10.63	1.67 ± 0.87

Environmental Conditions: During the pre-exposure and exposure phases in the tunnels, weather data were provided using a HOBO data logger placed inside the tunnels. The temperature was 62-124°F, the relative humidity was 19-100%, and rainfall occurred once (0.07 in on 1DAA). At the weather station during the exposure phase, the temperature was 56-98°F, the relative humidity was 27-100%, and recorded precipitation was 1.61 in. For the post-exposure phase, the temperature was -8 to 98°F, the relative humidity was 21-100%, and rainfall occurred each month with the greatest amount recorded in August.

Residues:

No sulfoxaflor or metabolite residues were detected in nectar, pollen, or whole plant samples prior to application. The parent material accounted for the majority of total residues in each matrix and treatment group (Tables 5-7). Across all treatments, parent material residues were greatest in whole plant samples and were relatively comparable between pollen and nectar. Whole plant samples were not analyzed for the metabolites. In Treatment 1, parent material residues in nectar, pollen, and whole plant samples ranged from 0.0383 to 0.441, <LOQ to 0.196, and 0.0565 to 1.31 mg/kg, respectively. In Treatment 2, parent material residues in nectar, pollen, and whole plant samples ranged from 0.0989 to 1.21, <LOD to 0.716, and 0.0522 to 2.50 mg/kg, respectively. The parent material residue peaked 1 or 2 DAA in each matrix and treatment level, and exhibited declines throughout the duration of the investigation period.

Table 6. Sulfoxaflor and metabolite residues in bee-collected buckwheat nectar.

DAL A	Sulfoxaflor (mg/kg)	X11519540 (mg/kg)	X11579457 (mg/kg)	X11721061 (mg/kg)	X11719474 (mg/kg)	Total Sulfoxaflor Residues (TSR) (mg/kg)
Treatment 1 (0.027 lb ai/A)						
-1	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD
1	--	0.0126	<LOD	0.00660	0.00670	0.0261
2	0.441	0.0186	<LOD	0.00410	0.0116	0.0475
3	0.100	0.00960	<LOD	0.00110	0.00820	0.119
4	0.0761	0.00450	<LOD	0.0015	0.00710	0.0894
7	0.0383	0.00390	<LOQ	<LOQ	0.0155	0.0587
Treatment 2 (0.065 lb ai/A)						
-1	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD
1	1.21	0.0137	<LOQ	0.0136	0.00930	1.25
2	1.10	0.0425	<LOQ	0.0131	0.0370	1.19
3	0.189	0.0112	<LOD	0.00240	0.0140	0.217
4	0.0989	0.00480	<LOD	0.00500	0.0100	0.119
7	0.200	0.0123	0.0011	0.0023	0.0491	0.265
Treatment 3 (0.083 lb ai/A)						
-1	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD
1	1.44	0.0283	0.00100	0.0168	0.0148	1.50
2	2.37	0.0738	0.00160	0.0225	0.0597	2.52
3	0.727	0.0328	<LOQ	0.00600	0.0317	0.798
4	0.240	0.0107	<LOQ	0.00170	0.0178	0.271
7	0.134	0.00940	<LOQ	0.00330	0.0438	0.191

LOQ = 0.001 mg/kg, LOD = 0.0003 mg/kg

Table 7. Sulfoxaflor and metabolite residues in bee-collected buckwheat pollen.

DAL A	Sulfoxaflor (mg/kg)	X11519540 (mg/kg)	X11579457 (mg/kg)	X11721061 (mg/kg)	X11719474 (mg/kg)	Total Sulfoxaflor Residues (TSR) (mg/kg)
Treatment 1 (0.027 lb ai/A)						
-1	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD
1	<LOQ	<LOD	<LOD	<LOD	<LOD	<LOQ
2	0.196	0.0117	<LOD	<LOD	<LOQ	0.216
3	0.155	0.0160	<LOD	<LOD	<LOQ	0.179
4	0.136	0.0162	<LOD	<LOD	<LOQ	0.161
7	0.0869	<LOQ	<LOD	<LOQ	0.0156	0.114
Treatment 2 (0.065 lb ai/A)						
-1	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD
0	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD
1	0.346	0.0144	<LOD	0.0121	<LOD	0.376
2	0.716	0.0669	<LOQ	0.0258	0.0243	0.838
3	0.265	0.0271	<LOD	<LOQ	0.0168	0.315
4	0.306	0.0399	<LOD	<LOQ	0.0233	0.376
7	0.298	0.0276	<LOD	<LOQ	0.0454	0.378
0.0276Treatment 3 (0.083 lb ai/A)						
-1	<LOD	<LOD	<LOD	<LOD	<LOD	<LOD
2	2.48	0.0297	0.0103	0.0533	0.134	2.71
3	0.364	0.0313	<LOD	<LOQ	0.0159	0.417
4	0.454	0.0381	<LOD	0.0115	0.0291	0.534
7	0.363	0.0277	<LOD	<LOQ	0.0527	0.450

LOQ = 0.001 mg/kg, LOD = 0.0003 mg/kg

DP Barcode: 447927

MRID No.: 50604601

Table 8. Sulfoxaflor residues (min/max) in buckwheat whole plants.

DAL A	Sulfoxaflor (mg/kg)
Treatment 1 (0.027 lb ai/A)	
-1	<LOD
0	1.31 (1.01, 1.53)
1	0.424
2	0.187
3	0.155
4	0.120
7	0.0565
Treatment 2 (0.065 lb ai/A)	
-1	<LOD
0	2.50 (1.66, 3.35)
1	1.17
2	0.0522
3	0.745
4	0.731
7	0.328
Treatment 3 (0.083 lb ai/A)	
-1	<LOD
0	3.80 (2.59, 6.15)
1	1.26
2	0.883
3	0.518
4	0.619
7	0.336

LOQ = 0.01 mg/kg, LOD = 0.003 mg/kg

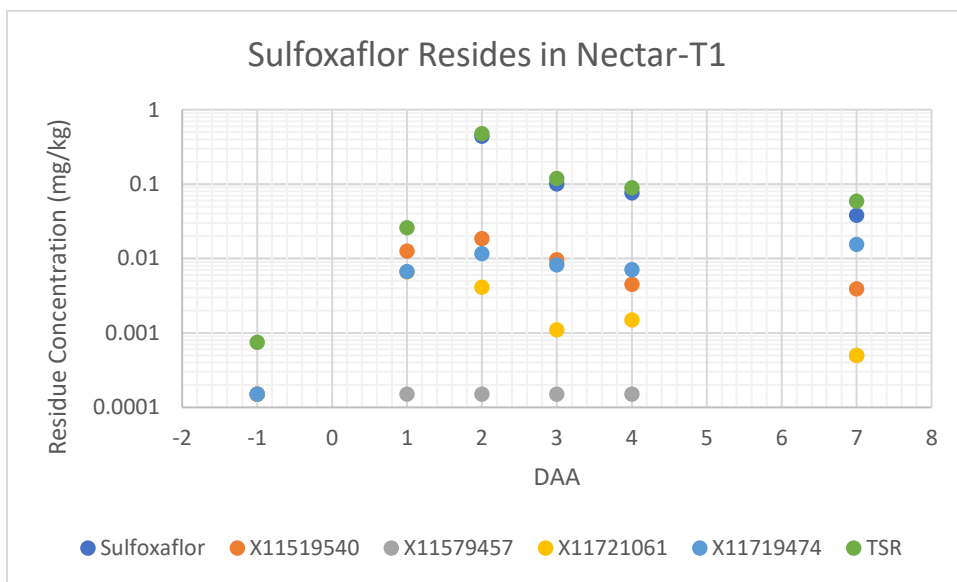


Figure 4. Sulfoxaflor, X11579457, X11719474, X11721061, X11519540 and total sulfoxaflor residues (TSR) in buckwheat nectar in Treatment 1.

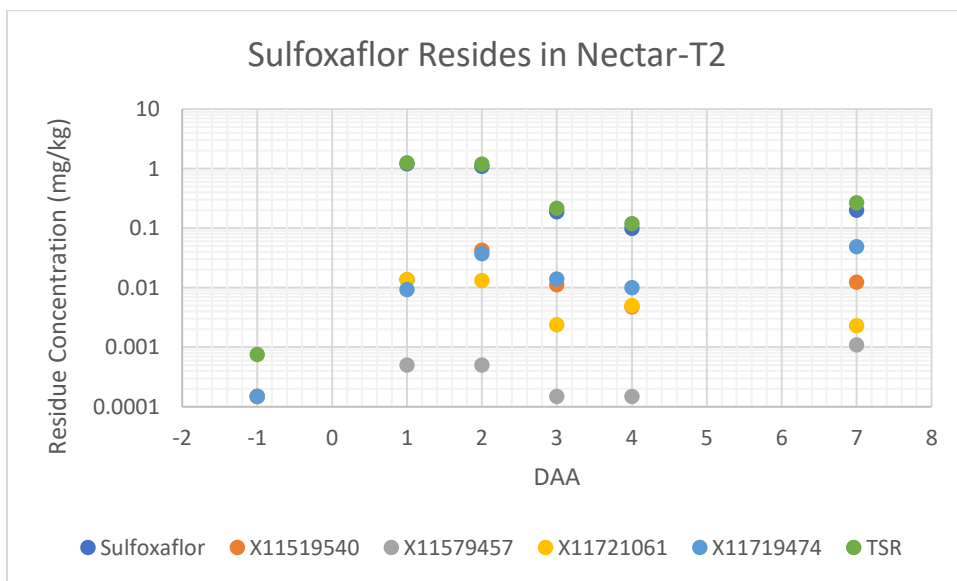


Figure 5. Sulfoxaflor, X11579457, X11719474, X11721061, X11519540 and total sulfoxaflor residues (TSR) in buckwheat nectar in Treatment 2.

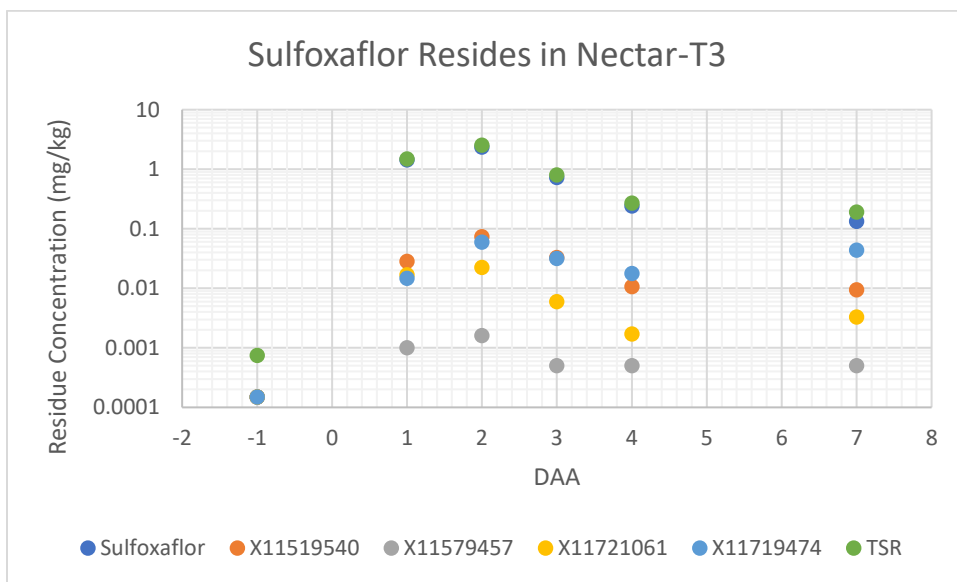


Figure 6. Sulfoxaflor, X11579457, X11719474, X11721061, X11519540 and total sulfoxaflor residues (TSR) in buckwheat nectar in Treatment 3.

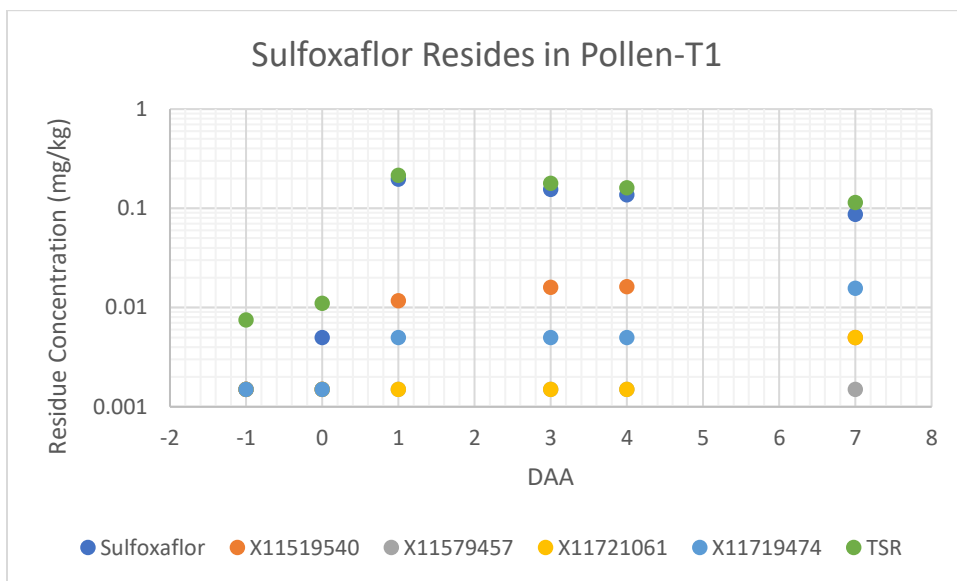


Figure 7. Sulfoxaflor, X11579457, X11719474, X11721061, X11519540 and total sulfoxaflor residues (TSR) in buckwheat pollen in Treatment 1.

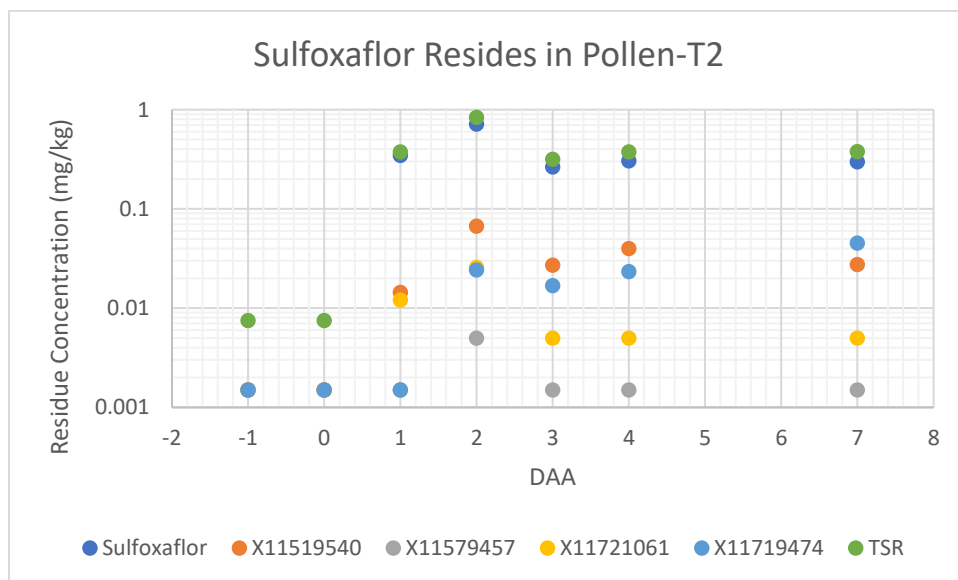


Figure 8. Sulfoxaflor, X11579457, X11719474, X11721061, X11519540 and total sulfoxaflor residues (TSR) in buckwheat pollen in Treatment 2.

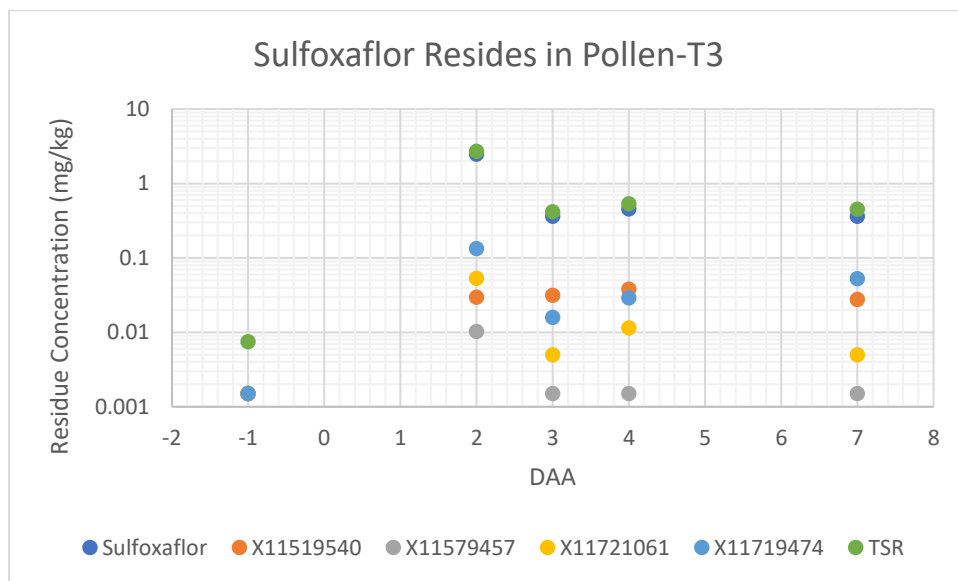


Figure 9. Sulfoxaflor, X11579457, X11719474, X11721061, X11519540 and total sulfoxaflor residues (TSR) in buckwheat pollen in Treatment 3.

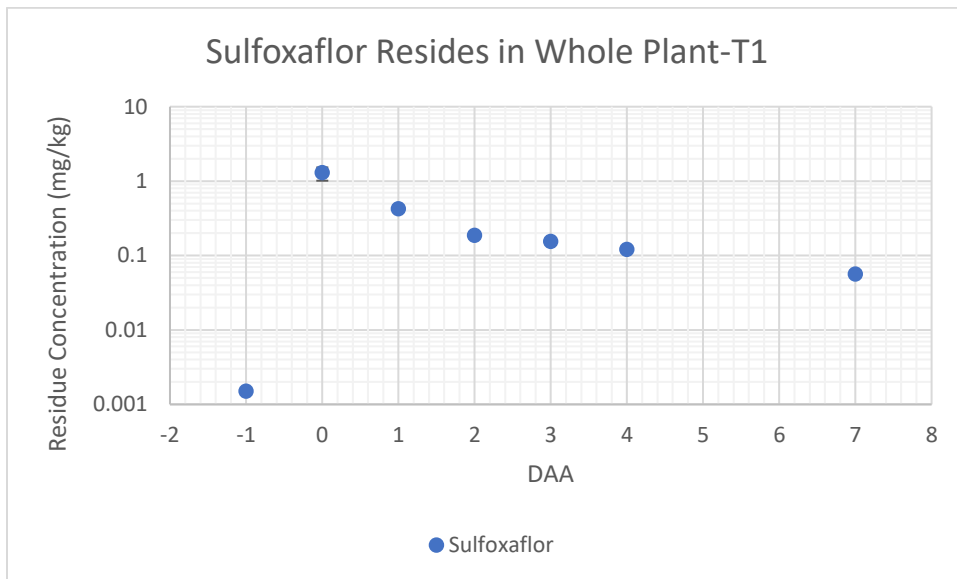


Figure 10. Sulfoxaflor in buckwheat whole plants in Treatment 1. Error bars represent the minimum and maximum replicate values.

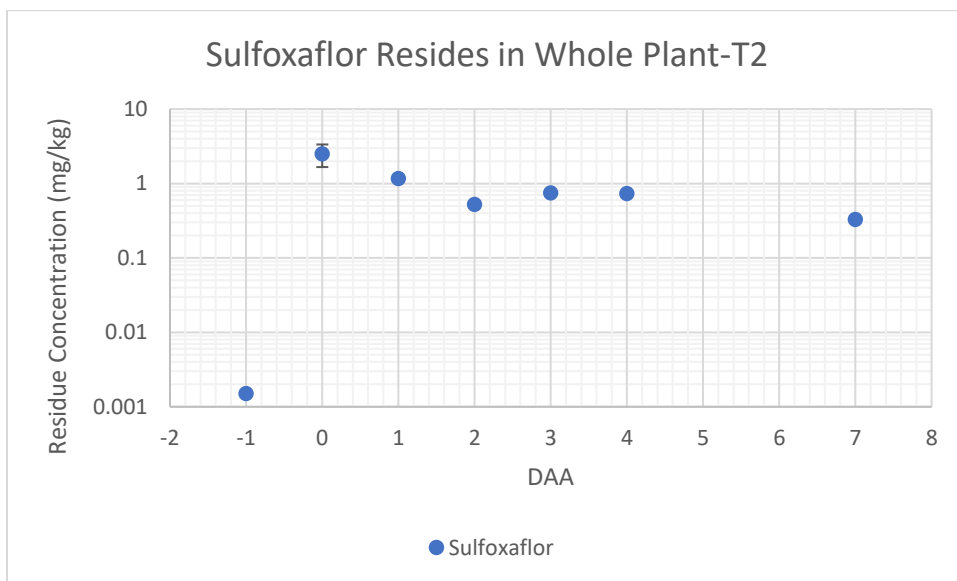


Figure 11. Sulfoxaflor in buckwheat whole plants in Treatment 2. Error bars represent the minimum and maximum replicate values.

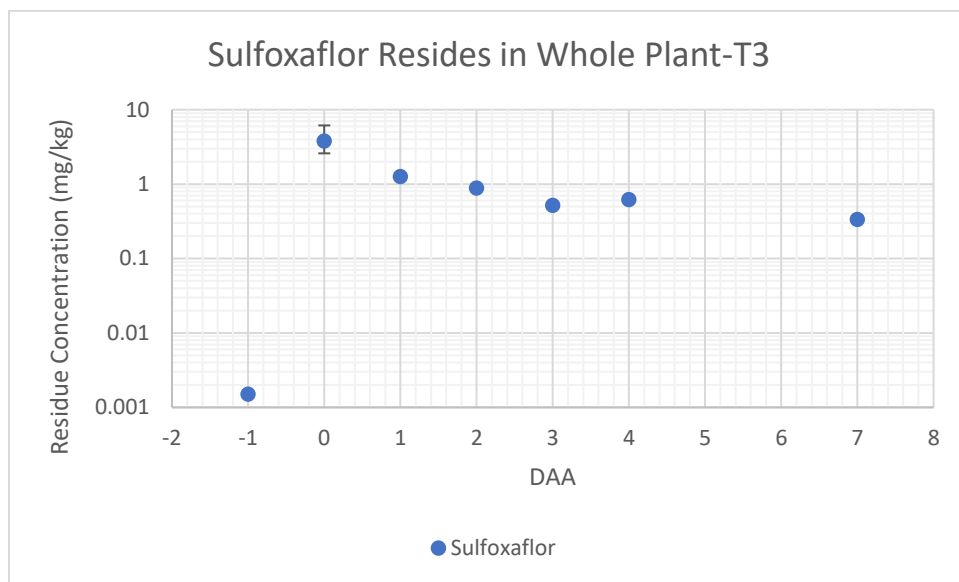


Figure 12. Sulfoxaflor in buckwheat whole plants in Treatment 3. Error bars represent the minimum and maximum replicate values.

REVIEWER'S CONSIDERATION OF STUDY STRENGTHS, LIMITATIONS, AND INTERPRETATION

It is important to recognize the inherent strengths and limitations of this study as results are interpreted and potentially considered in risk assessment.

In the context of available field studies involving honey bees, this study contains some strengths including:

- Inclusion of multiple colony-level endpoints reflecting hive condition, brood development, and nectar/pollen availability.
- Availability of raw data for conducting statistical analysis.
- Quantification of exposure to sulfoxaflor in the application solutions used to treat the crops.
- DT₅₀ values were estimated for the parent material in all matrices at each treatment level.

A number of limitations were noted, including:

- Samples for the residue portion were only collected for 7 days after application. As a consequence, the residue data represent a short observation period and residues were present at low levels at 7 days.
- Metabolites were not quantified in whole plant samples.
- Storage and transit stability of the residue samples collected were not determined.

- Overwintering survival was very poor in control hives which excludes use of that endpoint in analysis.

13. REVIEWER'S COMMENTS

Signed and Dated No Data Confidentiality, GLP, and Quality Assurance statements were provided. This study was conducted in compliance with the US EPA GLP regulations, with the exceptions of data connected to weather, agronomy and pesticide history, irrigation, maintenance chemical applications, GPS, validation of Honeybee Complete software, brood development photos, Nosema analysis, flower count, and flower count photos.

14. REFERENCES

OECD (2007) Guidance document on the honey bee (*Apis mellifera* L.) Brood test under semi-field conditions. Series on testing and assessment Number 75. ENV/JM/MONO(2007)22

Pistorius, J. et al. 2012. Effectiveness of method improvements to reduce variability of brood termination rate in honey bee brood studies under semi-field conditions. 11th International Symposium of the ICP-BR Bee Protection Group, Wageningen (The Netherlands), November 2-4, 2011. Julius Kuhn Archiv 437: 115-120.

UNITED STATES ENVIRONMENTAL PROTECTION AGENCY, Ecological Effects Test Guidelines OCSPP 850.3040, Field Testing for Pollinators, 2012.

APPENDIX A

R version 3.5.2 (2018-12-20) -- "Eggshell Igloo"
 Copyright (C) 2018 The R Foundation for Statistical Computing
 Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
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Type 'demo()' for some demos, 'help()' for on-line help, or
 'help.start()' for an HTML browser interface to help.
 Type 'q()' to quit R.

[Workspace loaded from ~/.RData]

```
library("dplyr")
library("ggpubr")
library('DescTools')
> Tunnel2<-read.csv(file='C:/Users/mniesen/Documents/Rwork/Tunnel/USTunnel2.csv', header=TRUE)
> Mort2<-read.csv(file='C:/Users/mniesen/Documents/Rwork/Tunnel/USMortality2.csv', header=TRUE)
> Forag2<-read.csv(file='C:/Users/mniesen/Documents/Rwork/Tunnel/USForaging2.csv', header=TRUE)
```

```
> with(Tunnel2, tapply(Adults, Day, shapiro.test))
$`-2DAA`
```

Shapiro-wilk normality test

```
data:  X[[i]]
W = 0.96697, p-value = 0.5465
```

```
$`26DAA`
```

Shapiro-wilk normality test

```
data:  X[[i]]
W = 0.94863, p-value = 0.2154
```

```
$`43DAA`
```

Shapiro-wilk normality test

```
data: x[[i]]  
w = 0.94399, p-value = 0.1672
```

```
$`8DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.96071, p-value = 0.4057
```

```
$Fall
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.90182, p-value = 0.02757
```

```
$Spring
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.9544, p-value = 0.7383
```

```
> with(Tunnel2, tapply(CapB, Day, shapiro.test))  
$`-2DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.98613, p-value = 0.9709
```

```
$`26DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.77868, p-value = 0.0001023
```

```
$`43DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]
```

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MRID No.: 50604601

w = 0.91804, p-value = 0.04045

\$`8DAA`

Shapiro-wilk normality test

data: x[[i]]

w = 0.96247, p-value = 0.4426

\$Fall

Shapiro-wilk normality test

data: x[[i]]

w = 0.97081, p-value = 0.7083

\$Spring

Shapiro-wilk normality test

data: x[[i]]

w = 0.84901, p-value = 0.09309

> with(Tunnel2, tapply(OpenB, Day, shapiro.test))

\$`-2DAA`

Shapiro-wilk normality test

data: x[[i]]

w = 0.94174, p-value = 0.1478

\$`26DAA`

Shapiro-wilk normality test

data: x[[i]]

w = 0.91119, p-value = 0.02808

\$`43DAA`

Shapiro-wilk normality test

data: x[[i]]

w = 0.94147, p-value = 0.1456

```
$`8DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
W = 0.94622, p-value = 0.1889
```

```
$Fall
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
W = 0.93207, p-value = 0.1213
```

```
$Spring
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
W = 0.88855, p-value = 0.2268
```

```
> with(Tunnel2, tapply(Honey, Day, shapiro.test))
```

```
$`-2DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
W = 0.98738, p-value = 0.9817
```

```
$`26DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
W = 0.95081, p-value = 0.2423
```

```
$`43DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
W = 0.95514, p-value = 0.3048
```

```
$`8DAA`
```

Shapiro-wilk normality test

data: X[[i]]
W = 0.97213, p-value = 0.679

\$Fall

Shapiro-wilk normality test

data: X[[i]]
W = 0.97214, p-value = 0.74

\$Spring

Shapiro-wilk normality test

data: X[[i]]
W = 0.89824, p-value = 0.242

```
> with(Tunnel2, tapply(Pollen, Day, shapiro.test))  
$`-2DAA`
```

Shapiro-wilk normality test

data: X[[i]]
W = 0.93882, p-value = 0.1259

\$`26DAA`

Shapiro-wilk normality test

data: X[[i]]
W = 0.92839, p-value = 0.07096

\$`43DAA`

Shapiro-wilk normality test

data: X[[i]]
W = 0.82866, p-value = 0.0005637

\$`8DAA`

Shapiro-wilk normality test

```
data: x[[i]]  
w = 0.82148, p-value = 0.0004179
```

```
$Fall
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.95244, p-value = 0.3285
```

```
$Spring
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.9577, p-value = 0.7879
```

```
> bartlett.test(Adults[Day=="-2DAA"] ~ Trt[Day=="-2DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Adults[Day == "-2DAA"] by Trt[Day == "-2DAA"]  
Bartlett's K-squared = 3.6856, df = 3, p-value = 0.2975
```

```
> bartlett.test(Adults[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Adults[Day == "8DAA"] by Trt[Day == "8DAA"]  
Bartlett's K-squared = 0.88475, df = 3, p-value = 0.8291
```

```
> bartlett.test(Adults[Day=="26DAA"] ~ Trt[Day=="26DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Adults[Day == "26DAA"] by Trt[Day == "26DAA"]  
Bartlett's K-squared = 0.74878, df = 3, p-value = 0.8617
```

```
> bartlett.test(Adults[Day=="43DAA"] ~ Trt[Day=="43DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Adults[Day == "43DAA"] by Trt[Day == "43DAA"]  
Bartlett's K-squared = 3.1879, df = 3, p-value = 0.3636
```

```
> bartlett.test(Adults[Day=="Fall"] ~ Trt[Day=="Fall"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Adults[Day == "Fall"] by Trt[Day == "Fall"]
Bartlett's K-squared = 6.5588, df = 3, p-value = 0.08737

> bartlett.test(Adults[Day=="Spring"] ~ Trt[Day=="Spring"], Tunnel2)
Error in bartlett.test.default(c(14045L, 11537L, 11474L, 3574L, 1129L,  :
  there must be at least 2 observations in each group
>
> bartlett.test(CapB[Day=="-2DAA"] ~ Trt[Day=="-2DAA"], Tunnel2)

    Bartlett test of homogeneity of variances

data: CapB[Day == "-2DAA"] by Trt[Day == "-2DAA"]
Bartlett's K-squared = 4.9447, df = 3, p-value = 0.1759

> bartlett.test(CapB[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel2)

    Bartlett test of homogeneity of variances

data: CapB[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 2.4999, df = 3, p-value = 0.4753

> bartlett.test(CapB[Day=="26DAA"] ~ Trt[Day=="26DAA"], Tunnel2)

    Bartlett test of homogeneity of variances

data: CapB[Day == "26DAA"] by Trt[Day == "26DAA"]
Bartlett's K-squared = 14.287, df = 3, p-value = 0.002539

> bartlett.test(CapB[Day=="43DAA"] ~ Trt[Day=="43DAA"], Tunnel2)

    Bartlett test of homogeneity of variances

data: CapB[Day == "43DAA"] by Trt[Day == "43DAA"]
Bartlett's K-squared = 6.5247, df = 3, p-value = 0.08869

> bartlett.test(CapB[Day=="Fall"] ~ Trt[Day=="Fall"], Tunnel2)

    Bartlett test of homogeneity of variances

data: CapB[Day == "Fall"] by Trt[Day == "Fall"]
Bartlett's K-squared = 3.6109, df = 3, p-value = 0.3067

> bartlett.test(CapB[Day=="Spring"] ~ Trt[Day=="Spring"], Tunnel2)
Error in bartlett.test.default(c(15466L, 15257L, 17556L, 627L, 20691L,  :
  there must be at least 2 observations in each group
>
> bartlett.test(OpenB[Day=="-2DAA"] ~ Trt[Day=="-2DAA"], Tunnel2)

    Bartlett test of homogeneity of variances
```

```
data: OpenB[Day == "-2DAA"] by Trt[Day == "-2DAA"]
Bartlett's K-squared = 1.6825, df = 3, p-value = 0.6408
```

```
> bartlett.test(OpenB[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: OpenB[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 5.9909, df = 3, p-value = 0.1121
```

```
> bartlett.test(OpenB[Day=="26DAA"] ~ Trt[Day=="26DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: OpenB[Day == "26DAA"] by Trt[Day == "26DAA"]
Bartlett's K-squared = 8.2644, df = 3, p-value = 0.04085
```

```
> bartlett.test(OpenB[Day=="43DAA"] ~ Trt[Day=="43DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: OpenB[Day == "43DAA"] by Trt[Day == "43DAA"]
Bartlett's K-squared = 5.6176, df = 3, p-value = 0.1318
```

```
> bartlett.test(OpenB[Day=="Fall"] ~ Trt[Day=="Fall"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: OpenB[Day == "Fall"] by Trt[Day == "Fall"]
Bartlett's K-squared = 4.1442, df = 3, p-value = 0.2463
```

```
> bartlett.test(OpenB[Day=="Spring"] ~ Trt[Day=="Spring"], Tunnel2)
Error in bartlett.test.default(c(23408L, 14003L, 20064L, 627L, 24035L, :
  there must be at least 2 observations in each group
```

```
>
```

```
> bartlett.test(Pollen[Day=="-2DAA"] ~ Trt[Day=="-2DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Pollen[Day == "-2DAA"] by Trt[Day == "-2DAA"]
Bartlett's K-squared = 4.4291, df = 3, p-value = 0.2187
```

```
> bartlett.test(Pollen[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Pollen[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 11.274, df = 3, p-value = 0.01033
```

```
> bartlett.test(Pollen[Day=="26DAA"] ~ Trt[Day=="26DAA"], Tunnel2)
```

Bartlett test of homogeneity of variances

data: Pollen[Day == "26DAA"] by Trt[Day == "26DAA"]
Bartlett's K-squared = 6.3474, df = 3, p-value = 0.09588

```
> bartlett.test(Pollen[Day=="43DAA"] ~ Trt[Day=="43DAA"], Tunnel2)
```

Bartlett test of homogeneity of variances

data: Pollen[Day == "43DAA"] by Trt[Day == "43DAA"]
Bartlett's K-squared = 6.7563, df = 3, p-value = 0.08008

```
> bartlett.test(Pollen[Day=="Fall"] ~ Trt[Day=="Fall"], Tunnel2)
```

Bartlett test of homogeneity of variances

data: Pollen[Day == "Fall"] by Trt[Day == "Fall"]
Bartlett's K-squared = 3.9996, df = 3, p-value = 0.2615

```
> bartlett.test(Pollen[Day=="Spring"] ~ Trt[Day=="Spring"], Tunnel2)
Error in bartlett.test.default(c(10659L, 7524L, 4598L, 7524L, 8151L, 1254L,
:
  there must be at least 2 observations in each group
>
> bartlett.test(Honey[Day=="-2DAA"] ~ Trt[Day=="-2DAA"], Tunnel2)
```

Bartlett test of homogeneity of variances

data: Honey[Day == "-2DAA"] by Trt[Day == "-2DAA"]
Bartlett's K-squared = 1.1389, df = 3, p-value = 0.7677

```
> bartlett.test(Honey[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel2)
```

Bartlett test of homogeneity of variances

data: Honey[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 1.5804, df = 3, p-value = 0.6639

```
> bartlett.test(Honey[Day=="26DAA"] ~ Trt[Day=="26DAA"], Tunnel2)
```

Bartlett test of homogeneity of variances

data: Honey[Day == "26DAA"] by Trt[Day == "26DAA"]
Bartlett's K-squared = 1.0243, df = 3, p-value = 0.7954

```
> bartlett.test(Honey[Day=="43DAA"] ~ Trt[Day=="43DAA"], Tunnel2)
```

Bartlett test of homogeneity of variances

data: Honey[Day == "43DAA"] by Trt[Day == "43DAA"]
Bartlett's K-squared = 1.3232, df = 3, p-value = 0.7236

```
> bartlett.test(Honey[Day=="Fall"] ~ Trt[Day=="Fall"], Tunnel2)
```

Bartlett test of homogeneity of variances

```
data: Honey[Day == "Fall"] by Trt[Day == "Fall"]
Bartlett's K-squared = 2.2254, df = 3, p-value = 0.527
```

```
> bartlett.test(Honey[Day=="Spring"] ~ Trt[Day=="Spring"], Tunnel2)
Error in bartlett.test.default(c(29678L, 26334L, 28842L, 22781L, 61028L, :
  there must be at least 2 observations in each group
```

```
> DunnettTest(Adults~Trt, data=Tunnel2[Tunnel2$Day=='-2DAA',])
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

```
$Cont
      diff      lwr.ci      upr.ci    pval
T1-Cont -522.6667 -2849.573 1804.2392 0.9012
T2-Cont -1515.1667 -3842.073  811.7392 0.2672
T3-Cont -2456.0000 -4782.906 -129.0941 0.0370 *
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Adults~Trt, data=Tunnel2[Tunnel2$Day=='8DAA',])
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

```
$Cont
      diff      lwr.ci      upr.ci    pval
T1-Cont -566.9583 -3966.127 2832.21 0.9552
T2-Cont -389.4583 -3788.627 3009.71 0.9845
T3-Cont -1298.4583 -4697.627 2100.71 0.6676
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Adults~Trt, data=Tunnel2[Tunnel2$Day=='26DAA',])
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

```
$Cont
      diff      lwr.ci      upr.ci    pval
T1-Cont -1755.50000 -3534.558  23.55806 0.0539 .
T2-Cont  -31.33333 -1810.391 1747.72473 0.9999
T3-Cont   52.16667 -1726.891 1831.22473 0.9997
```

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel2[Tunnel2$Day=='43DAA',])

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -1523.083 -5859.731 2813.565 0.7192
T2-Cont -3299.583 -7636.231 1037.065 0.1653
T3-Cont -1094.583 -5431.231 3242.065 0.8677

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CapB~Trt, data=Tunnel2[Tunnel2$Day=='-2DAA',])

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont  322.2083 -4279.585 4924.002 0.9963
T2-Cont 1123.3750 -3478.419 5725.169 0.8782
T3-Cont  496.3750 -4105.419 5098.169 0.9869

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CapB~Trt, data=Tunnel2[Tunnel2$Day=='8DAA',])

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -4075.50000 -9370.005 1219.005 0.1590
T2-Cont   34.83333 -5259.671 5329.338 1.0000
T3-Cont -6479.00000 -11773.505 -1184.495 0.0143 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CapB~Trt, data=Tunnel2[Tunnel2$Day=='Fall',])

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

$Cont

```

	diff	lwr.ci	upr.ci	pval
T1-Cont	2129.810	-5530.093	9789.712	0.8279
T2-Cont	-1074.857	-9136.672	6986.958	0.9751
T3-Cont	2227.343	-5834.472	10289.158	0.8306

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>

```
> DunnettTest(OpenB~Trt, data=Tunnel2[Tunnel2$Day=='-2DAA',])
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	-121.9167	-6008.069	5764.235	0.9999
T2-Cont	-1898.4167	-7784.569	3987.735	0.7658
T3-Cont	-2386.0833	-8272.235	3500.069	0.6279

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> DunnettTest(OpenB~Trt, data=Tunnel2[Tunnel2$Day=='8DAA',])
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	-6844.75	-14084.741	395.2415	0.0670 .
T2-Cont	470.25	-6769.741	7710.2415	0.9970
T3-Cont	-2978.25	-10218.241	4261.7415	0.6178

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> DunnettTest(OpenB~Trt, data=Tunnel2[Tunnel2$Day=='43DAA',])
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	7628.500	-1722.143	16979.143	0.1280
T2-Cont	1950.667	-7399.976	11301.310	0.9185
T3-Cont	-1463.000	-10813.643	7887.643	0.9625

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> DunnettTest(OpenB~Trt, data=Tunnel2[Tunnel2$Day=='Fall'],)
```

```
Dunnett's test for comparing several treatments with a control :
  95% family-wise confidence level
```

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont 2373.643 -3546.9462 8294.232 0.6281
T2-Cont 6449.143  217.9027 12680.383 0.0414 *
T3-Cont 4609.943 -1621.2973 10841.183 0.1790
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
>
> DunnettTest(Pollen~Trt, data=Tunnel2[Tunnel2$Day=='-2DAA'],)
```

```
Dunnett's test for comparing several treatments with a control :
  95% family-wise confidence level
```

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -2177.0833 -5401.447 1047.280 0.2419
T2-Cont -1306.2500 -4530.614 1918.114 0.6283
T3-Cont   748.9167 -2475.447 3973.280 0.8925
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Pollen~Trt, data=Tunnel2[Tunnel2$Day=='26DAA'],)
```

```
Dunnett's test for comparing several treatments with a control :
  95% family-wise confidence level
```

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -1227.875 -4856.142 2400.392 0.7402
T2-Cont -2133.542 -5761.808 1494.725 0.3437
T3-Cont   26.125 -3602.142 3654.392 1.0000
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Pollen~Trt, data=Tunnel2[Tunnel2$Day=='Fall'],)
```

```
Dunnett's test for comparing several treatments with a control :
  95% family-wise confidence level
```

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -746.4286 -4864.821 3371.964 0.9418
```

T2-Cont 2890.1714 -1444.312 7224.654 0.2459
 T3-Cont 925.5714 -3408.912 5260.054 0.9104

 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
 > DunnettTest(Honey~Trt, data=Tunnel2[Tunnel2\$Day=='-2DAA',])

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

\$Cont		diff	lwr.ci	upr.ci	pval
T1-Cont	1480.417	-4155.173	7116.006	0.8541	
T2-Cont	-2177.083	-7812.673	3458.506	0.6603	
T3-Cont	-3013.083	-8648.673	2622.506	0.4185	

 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Honey~Trt, data=Tunnel2[Tunnel2\$Day=='8DAA',])

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

\$Cont		diff	lwr.ci	upr.ci	pval
T1-Cont	1628.458	-4646.510	7903.427	0.8583	
T2-Cont	1489.125	-4785.844	7764.094	0.8865	
T3-Cont	-2342.542	-8617.510	3932.427	0.6823	

 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Honey~Trt, data=Tunnel2[Tunnel2\$Day=='26DAA',])

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

\$Cont		diff	lwr.ci	upr.ci	pval
T1-Cont	2325.125	-5591.472	10241.7221	0.8101	
T2-Cont	-4223.542	-12140.139	3693.0554	0.4201	
T3-Cont	-7288.875	-15205.472	627.7221	0.0757 .	

 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Honey~Trt, data=Tunnel2[Tunnel2\$Day=='43DAA',])

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -3378.833 -11545.83  4788.166 0.61367
T2-Cont -12191.667 -20358.67 -4024.667 0.00285 **
T3-Cont -14212.000 -22379.00 -6045.001 0.00067 ***
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Honey~Trt, data=Tunnel2[Tunnel2$Day=='Fall'],)
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont  5921.667 -13445.81 25289.14 0.7862
T2-Cont -5601.200 -25984.88 14782.48 0.8327
T3-Cont   250.800 -20132.88 20634.48 1.0000
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> with(Tunnel2[Tunnel2$Day=="Fall",], pairwise.wilcox.test(Adults, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Adults and Trt

```
Cont T1 T2
T1 1 - -
T2 1 1 -
T3 1 1 1
```

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
```

```
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
```

```
> with(Tunnel2[Tunnel2$Day=="26DAA",], pairwise.wilcox.test(CapB, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: CapB and Trt

	Cont	T1	T2
T1	1.00	-	-
T2	1.00	1.00	-
T3	1.00	0.17	0.72

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel2[Tunnel2$Day=="43DAA",], pairwise.wilcox.test(CapB, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: CapB and Trt

	Cont	T1	T2
T1	1	-	-
T2	1	1	-
T3	1	1	1

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel2[Tunnel2$Day=="26DAA",], pairwise.wilcox.test(OpenB, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: OpenB and Trt

	Cont	T1	T2
T1	0.022	-	-
T2	1.000	1.000	-
T3	1.000	0.147	1.000

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel2[Tunnel2$Day=="43DAA",], pairwise.wilcox.test(Pollen, Trt, p.adj
j = 'bonf'))

```

Pairwise comparisons using wilcoxon rank sum test

data: Pollen and Trt

	Cont	T1	T2
T1	1	-	-
T2	1	1	-
T3	1	1	1

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel2[Tunnel2$Day=="8DAA",], pairwise.wilcox.test(Pollen, Trt, p.adj
= 'bonf'))

```

Pairwise comparisons using wilcoxon rank sum test

data: Pollen and Trt

	Cont	T1	T2
T1	1.00	-	-
T2	1.00	0.32	-
T3	1.00	1.00	0.32

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :

```

```

cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties

```

```

> with(Mort2, tapply(Mortality, Day, shapiro.test))
$`0DAA`

```

Shapiro-wilk normality test

```

data:  x[[i]]
W = 0.87377, p-value = 0.004263

```

```

$`1DAA`

```

Shapiro-wilk normality test

```

data:  x[[i]]
W = 0.88191, p-value = 0.006318

```

```

$`1DBA`

```

Shapiro-wilk normality test

```

data:  x[[i]]
W = 0.92663, p-value = 0.06445

```

```

$`2DAA`

```

Shapiro-wilk normality test

```

data:  x[[i]]
W = 0.86813, p-value = 0.003263

```

```

$`3DAA`

```

Shapiro-wilk normality test

```

data:  x[[i]]
W = 0.89773, p-value = 0.01394

```

\$`4DAA`

Shapiro-wilk normality test

data: x[[i]]
W = 0.68322, p-value = 3.151e-06

\$`5DAA`

Shapiro-wilk normality test

data: x[[i]]
W = 0.82859, p-value = 0.0005621

\$`6DAA`

Shapiro-wilk normality test

data: x[[i]]
W = 0.93018, p-value = 0.07826

\$`7DAA`

Shapiro-wilk normality test

data: x[[i]]
W = 0.82189, p-value = 0.000425

\$`8DAA`

Shapiro-wilk normality test

data: x[[i]]
W = 0.96071, p-value = 0.4056

\$`9DAA`

Shapiro-wilk normality test

data: x[[i]]
W = 0.75521, p-value = 3.336e-05

```
> bartlett.test(Mortality[Day=="0DAA"] ~ Trt[Day=="0DAA"], Mort2)
```

Bartlett test of homogeneity of variances

data: Mortality[Day == "0DAA"] by Trt[Day == "0DAA"]
Bartlett's K-squared = 45.114, df = 3, p-value = 8.749e-10

```
> bartlett.test(Mortality[Day=="1DAA"] ~ Trt[Day=="1DAA"], Mort2)
```

Bartlett test of homogeneity of variances

data: Mortality[Day == "1DAA"] by Trt[Day == "1DAA"]
Bartlett's K-squared = 14.791, df = 3, p-value = 0.002004

```
> bartlett.test(Mortality[Day=="2DAA"] ~ Trt[Day=="2DAA"], Mort2)
```

Bartlett test of homogeneity of variances

data: Mortality[Day == "2DAA"] by Trt[Day == "2DAA"]
Bartlett's K-squared = 11.439, df = 3, p-value = 0.009572

```
> bartlett.test(Mortality[Day=="3DAA"] ~ Trt[Day=="3DAA"], Mort2)
```

Bartlett test of homogeneity of variances

data: Mortality[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 9.5911, df = 3, p-value = 0.02238

```
> bartlett.test(Mortality[Day=="4DAA"] ~ Trt[Day=="4DAA"], Mort2)
```

Bartlett test of homogeneity of variances

data: Mortality[Day == "4DAA"] by Trt[Day == "4DAA"]
Bartlett's K-squared = 18.59, df = 3, p-value = 0.0003323

```
> bartlett.test(Mortality[Day=="5DAA"] ~ Trt[Day=="5DAA"], Mort2)
```

Bartlett test of homogeneity of variances

data: Mortality[Day == "5DAA"] by Trt[Day == "5DAA"]
Bartlett's K-squared = 11.774, df = 3, p-value = 0.0082

```
> bartlett.test(Mortality[Day=="6DAA"] ~ Trt[Day=="6DAA"], Mort2)
```

Bartlett test of homogeneity of variances

data: Mortality[Day == "6DAA"] by Trt[Day == "6DAA"]
Bartlett's K-squared = 2.3307, df = 3, p-value = 0.5067

```
> bartlett.test(Mortality[Day=="7DAA"] ~ Trt[Day=="7DAA"], Mort2)
```

Bartlett test of homogeneity of variances

```
data: Mortality[Day == "7DAA"] by Trt[Day == "7DAA"]
Bartlett's K-squared = 7.3476, df = 3, p-value = 0.06161
```

```
> bartlett.test(Mortality[Day=="8DAA"] ~ Trt[Day=="8DAA"], Mort2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Mortality[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 0.38565, df = 3, p-value = 0.9432
```

```
> bartlett.test(Mortality[Day=="9DAA"] ~ Trt[Day=="9DAA"], Mort2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Mortality[Day == "9DAA"] by Trt[Day == "9DAA"]
Bartlett's K-squared = 18.671, df = 3, p-value = 0.0003197
```

```
> DunnettTest(Mortality~Trt, data=Mort2[Mort2$Day=='6DAA',])
```

```
Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level
```

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -5.87500 -20.613892  8.863892 0.6394
T2-Cont  2.12500 -12.613892 16.863892 0.9701
T3-Cont 10.29167  -4.447225 25.030558 0.2188
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Mortality~Trt, data=Mort2[Mort2$Day=='8DAA',])
```

```
Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level
```

```
$Cont
      diff      lwr.ci      upr.ci      pval
T1-Cont -1.708333 -21.57219 18.155522 0.9932
T2-Cont -13.708333 -33.57219  6.155522 0.2266
T3-Cont -18.208333 -38.07219  1.655522 0.0773 .
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> with(Mort2[Mort2$Day=="0DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

```
Pairwise comparisons using wilcoxon rank sum test
```

data: Mortality and Trt

	Cont	T1	T2
T1	0.014	-	-
T2	0.014	1.000	-
T3	0.014	0.013	0.030

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="1DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	0.070	-	-
T2	0.022	1.000	-
T3	0.014	0.558	0.558

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="2DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	0.701	-	-
T2	1.000	0.323	-

T3 0.020 0.052 0.753

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="3DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	0.55	-	-
T2	1.00	0.12	-
T3	1.00	0.18	1.00

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="4DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	1.000	-	-
T2	0.048	0.261	-
T3	1.000	1.000	0.765

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="5DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	0.42	-	-
T2	0.12	1.00	-
T3	0.56	1.00	1.00

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="1DBA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	0.65	-	-
T2	0.23	1.00	-
T3	1.00	1.00	1.00

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="7DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	1.00	-	-
T2	1.00	1.00	-
T3	1.00	0.89	1.00

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort2[Mort2$Day=="9DAA",], pairwise.wilcox.test(Mortality, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Mortality and Trt

	Cont	T1	T2
T1	1.000	-	-
T2	0.022	1.000	-
T3	1.000	1.000	0.049

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
```

```
cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
```

```
> with(Forag2, tapply(Foraging, Day, shapiro.test))
$`0DAA`
```

```
Shapiro-wilk normality test
```

```
data:  x[[i]]
W = 0.78924, p-value = 0.0001162
```

```
$`0DBA`
```

```
Shapiro-wilk normality test
```

```
data:  x[[i]]
W = 0.94732, p-value = 0.2005
```

```
$`1DAA`
```

```
Shapiro-wilk normality test
```

```
data:  x[[i]]
W = 0.97239, p-value = 0.686
```

```
$`1DBA`
```

```
Shapiro-wilk normality test
```

```
data:  x[[i]]
W = 0.87013, p-value = 0.003587
```

```
$`2DAA`
```

```
Shapiro-wilk normality test
```

```
data:  x[[i]]
W = 0.83226, p-value = 0.0006565
```

```
$`2DBA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.8034, p-value = 0.0002013
```

```
$`3DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.90541, p-value = 0.02072
```

```
$`4DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.94406, p-value = 0.1679
```

```
$`5DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.85205, p-value = 0.001559
```

```
$`6DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.86536, p-value = 0.002867
```

```
$`7DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.93088, p-value = 0.08133
```

```
$`8DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
w = 0.84939, p-value = 0.001384
```

```
$`9DAA`
```

```
Shapiro-wilk normality test
```

```
data: x[[i]]  
W = 0.88597, p-value = 0.007714
```

```
> bartlett.test(Foraging[Day=="0DBA"] ~ Trt[Day=="0DBA"], Forag2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Foraging[Day == "0DBA"] by Trt[Day == "0DBA"]  
Bartlett's K-squared = 4.6335, df = 3, p-value = 0.2007
```

```
> bartlett.test(Foraging[Day=="1DBA"] ~ Trt[Day=="1DBA"], Forag2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Foraging[Day == "1DBA"] by Trt[Day == "1DBA"]  
Bartlett's K-squared = 5.0612, df = 3, p-value = 0.1674
```

```
> bartlett.test(Foraging[Day=="2DBA"] ~ Trt[Day=="2DBA"], Forag2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Foraging[Day == "2DBA"] by Trt[Day == "2DBA"]  
Bartlett's K-squared = 6.568, df = 3, p-value = 0.08702
```

```
> bartlett.test(Foraging[Day=="0DAA"] ~ Trt[Day=="0DAA"], Forag2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Foraging[Day == "0DAA"] by Trt[Day == "0DAA"]  
Bartlett's K-squared = 10.954, df = 3, p-value = 0.01198
```

```
> bartlett.test(Foraging[Day=="1DAA"] ~ Trt[Day=="1DAA"], Forag2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Foraging[Day == "1DAA"] by Trt[Day == "1DAA"]  
Bartlett's K-squared = 8.7599, df = 3, p-value = 0.03266
```

```
> bartlett.test(Foraging[Day=="2DAA"] ~ Trt[Day=="2DAA"], Forag2)
```

```
Bartlett test of homogeneity of variances
```

```
data: Foraging[Day == "2DAA"] by Trt[Day == "2DAA"]  
Bartlett's K-squared = 20.568, df = 3, p-value = 0.0001294
```

```
> bartlett.test(Foraging[Day=="3DAA"] ~ Trt[Day=="3DAA"], Forag2)
```

```
    Bartlett test of homogeneity of variances
```

```
data:  Foraging[Day == "3DAA"] by Trt[Day == "3DAA"]  
Bartlett's K-squared = 3.5402, df = 3, p-value = 0.3156
```

```
> bartlett.test(Foraging[Day=="4DAA"] ~ Trt[Day=="4DAA"], Forag2)
```

```
    Bartlett test of homogeneity of variances
```

```
data:  Foraging[Day == "4DAA"] by Trt[Day == "4DAA"]  
Bartlett's K-squared = 3.9529, df = 3, p-value = 0.2666
```

```
> bartlett.test(Foraging[Day=="5DAA"] ~ Trt[Day=="5DAA"], Forag2)
```

```
    Bartlett test of homogeneity of variances
```

```
data:  Foraging[Day == "5DAA"] by Trt[Day == "5DAA"]  
Bartlett's K-squared = 7.4575, df = 3, p-value = 0.05866
```

```
> bartlett.test(Foraging[Day=="6DAA"] ~ Trt[Day=="6DAA"], Forag2)
```

```
    Bartlett test of homogeneity of variances
```

```
data:  Foraging[Day == "6DAA"] by Trt[Day == "6DAA"]  
Bartlett's K-squared = 10.306, df = 3, p-value = 0.01614
```

```
> bartlett.test(Foraging[Day=="7DAA"] ~ Trt[Day=="7DAA"], Forag2)
```

```
    Bartlett test of homogeneity of variances
```

```
data:  Foraging[Day == "7DAA"] by Trt[Day == "7DAA"]  
Bartlett's K-squared = 3.7893, df = 3, p-value = 0.2851
```

```
> bartlett.test(Foraging[Day=="8DAA"] ~ Trt[Day=="8DAA"], Forag2)
```

```
    Bartlett test of homogeneity of variances
```

```
data:  Foraging[Day == "8DAA"] by Trt[Day == "8DAA"]  
Bartlett's K-squared = 10.177, df = 3, p-value = 0.01712
```

```
> bartlett.test(Foraging[Day=="9DAA"] ~ Trt[Day=="9DAA"], Forag2)
```

```
    Bartlett test of homogeneity of variances
```

```
data:  Foraging[Day == "9DAA"] by Trt[Day == "9DAA"]  
Bartlett's K-squared = 8.3597, df = 3, p-value = 0.03913
```

```
> with(Forag2[Forag2$Day=="0DBA",], DunnettTest(Foraging~Trt))
```

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	0.4441667	-2.551212	3.4395452	0.9677
T2-Cont	-3.2758333	-6.271212	-0.2804548	0.0298 *
T3-Cont	-1.6108333	-4.606212	1.3845452	0.4139

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag2[Forag2\$Day=="4DAA",], DunnettTest(Foraging~Trt))

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	-2.112500	-3.502317	-0.722683	0.0025 **
T2-Cont	-3.724167	-5.113984	-2.334350	1.9e-06 ***
T3-Cont	-3.555833	-4.945650	-2.166016	6.5e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag2[Forag2\$Day=="7DAA",], DunnettTest(Foraging~Trt))

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	-1.737083	-2.707494	-0.7666726	0.00049 ***
T2-Cont	-1.237083	-2.207494	-0.2666726	0.01052 *
T3-Cont	-1.568750	-2.539161	-0.5983392	0.00139 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag2[Forag2\$Day=="1DBA",], pairwise.wilcox.test(Foraging, Trt, p.adj = 'bonf'))

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	1.00	-	-
T2	1.00	1.00	-
T3	1.00	0.63	1.00

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="2DBA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	1	-	-
T2	1	1	-
T3	1	1	1

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="0DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.014	-	-
T2	0.004	1.000	-

T3 0.004 0.147 0.052

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="1DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.63	-	-
T2	1.00	1.00	-
T3	0.27	0.39	1.00

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="2DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))
```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.014	-	-
T2	0.014	0.074	-
T3	0.014	0.111	1.000

P value adjustment method: bonferroni

Warning messages:

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
```

```

cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="3DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))

```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.014	-	-
T2	0.014	1.000	-
T3	0.014	1.000	0.147

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="5DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))

```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.142	-	-
T2	0.197	1.000	-
T3	0.022	0.179	0.379

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties

```

```

2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="6DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))

```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.014	-	-
T2	0.014	0.144	-
T3	0.021	1.000	1.000

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="8DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))

```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.004	-	-
T2	0.014	0.263	-
T3	0.014	1.000	0.095

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :

```

```

cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag2[Forag2$Day=="9DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))

```

Pairwise comparisons using wilcoxon rank sum test

data: Foraging and Trt

	Cont	T1	T2
T1	0.014	-	-
T2	0.070	0.390	-
T3	0.070	0.092	1.000

P value adjustment method: bonferroni

Warning messages:

```

1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
4: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
5: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
6: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties

```

```
> with(Brood1T3, shapiro.test(Tregg))
```

Shapiro-wilk normality test

data: Tregg

W = 0.96206, p-value = 0.4338

```
> with(Brood1T3, shapiro.test(Biegg))
```

Shapiro-wilk normality test

data: Biegg

W = 0.96196, p-value = 0.4315

```
> with(Brood1T3, shapiro.test(Ciegg))
```

Shapiro-wilk normality test

data: Ciegg
w = 0.97208, p-value = 0.6778

```
> with(Brood2T3, shapiro.test(Tregg))
```

Shapiro-wilk normality test

data: Tregg
w = 0.94179, p-value = 0.2155

```
> with(Brood2T3, shapiro.test(Biegg))
```

Shapiro-wilk normality test

data: Biegg
w = 0.90353, p-value = 0.03499

```
> with(Brood2T3, shapiro.test(Ciegg))
```

Shapiro-wilk normality test

data: Ciegg
w = 0.92028, p-value = 0.07704

```
> bartlett.test(Tregg ~ Trt, Brood1T3)
```

Bartlett test of homogeneity of variances

data: Tregg by Trt
Bartlett's K-squared = 1.2501, df = 3, p-value = 0.741

```
> bartlett.test(Biegg ~ Trt, Brood1T3)
```

Bartlett test of homogeneity of variances

data: Biegg by Trt
Bartlett's K-squared = 1.2578, df = 3, p-value = 0.7392

```
> bartlett.test(Ciegg ~ Trt, Brood1T3)
```

Bartlett test of homogeneity of variances

data: Ciegg by Trt
Bartlett's K-squared = 0.95461, df = 3, p-value = 0.8122

```
> bartlett.test(Tregg ~ Trt, Brood2T3)
```

Bartlett test of homogeneity of variances

data: Tregg by Trt
 Bartlett's K-squared = 2.2644, df = 3, p-value = 0.5194

```
> bartlett.test(Biegg ~ Trt, Brood2T3)
```

Bartlett test of homogeneity of variances

data: Biegg by Trt
 Bartlett's K-squared = 2.71, df = 3, p-value = 0.4385

```
> bartlett.test(Ciegg ~ Trt, Brood2T3)
```

Bartlett test of homogeneity of variances

data: Ciegg by Trt
 Bartlett's K-squared = 0.91605, df = 3, p-value = 0.8216

```
> DunnettTest(Tregg, Trt, data=Brood1T3)
```

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

\$Cont		diff	lwr.ci	upr.ci	pval
T1-Cont	15.17792	-13.9798741	44.33571	0.4397	
T2-Cont	11.11125	-18.0465407	40.26904	0.6692	
T3-Cont	29.02958	-0.1282074	58.18737	0.0511 .	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> DunnettTest(Biegg, Trt, data=Brood1T3)
```

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

\$Cont		diff	lwr.ci	upr.ci	pval
T1-Cont	-0.760	-2.218806	0.698805548	0.4390	
T2-Cont	-0.555	-2.013806	0.903805548	0.6702	
T3-Cont	-1.450	-2.908806	0.008805548	0.0516 .	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> DunnettTest(Ciegg, Trt, data=Brood1T3)
```

Dunnett's test for comparing several treatments with a control :
 95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	-0.4137500	-1.914774	1.0872738	0.8363
T2-Cont	-0.6404167	-2.141440	0.8606072	0.5918
T3-Cont	-1.3004167	-2.801440	0.2006072	0.0997 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Tregg, Trt, data=Brood2T3)

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	4.078571	-9.444826	17.601969	0.7926
T2-Cont	2.033571	-13.201907	17.269050	0.9750
T3-Cont	-5.579429	-19.812393	8.653536	0.6431

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Biegg, Trt, data=Brood2T3)

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	-0.390	-0.9684392	0.1884392	0.2379
T2-Cont	-0.190	-0.8416704	0.4616704	0.8080
T3-Cont	0.214	-0.3947897	0.8227897	0.7119

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

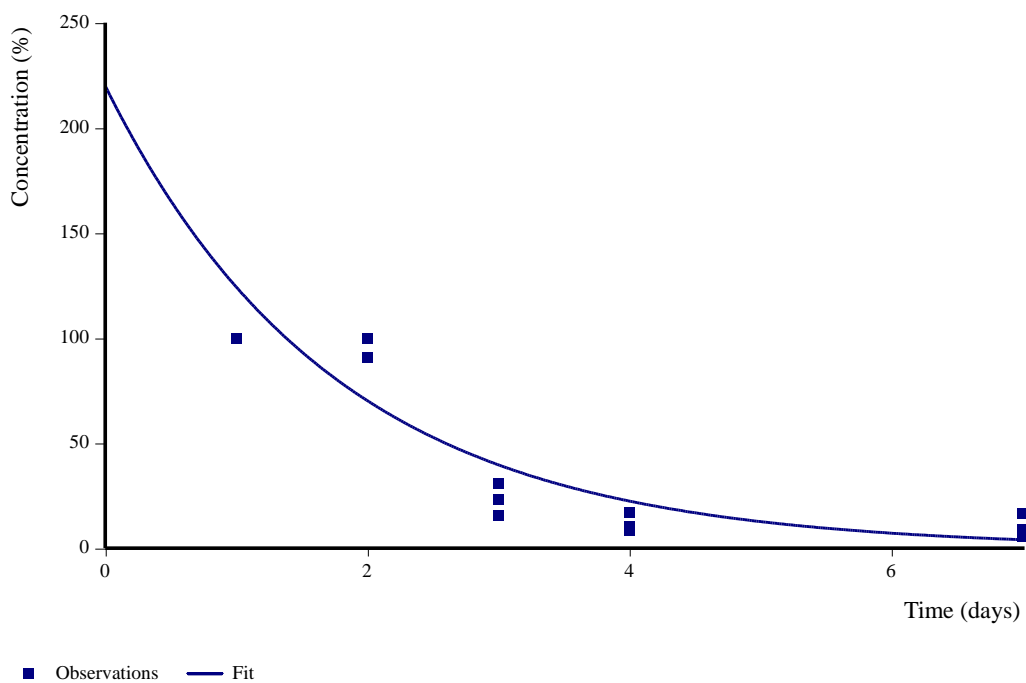
> DunnettTest(Ciegg, Trt, data=Brood2T3)

Dunnett's test for comparing several treatments with a control :
95% family-wise confidence level

\$Cont

	diff	lwr.ci	upr.ci	pval
T1-Cont	-0.2316667	-0.7183189	0.2549856	0.5017
T2-Cont	-0.1275000	-0.6757631	0.4207631	0.8886
T3-Cont	0.1900000	-0.3221867	0.7021867	0.6790

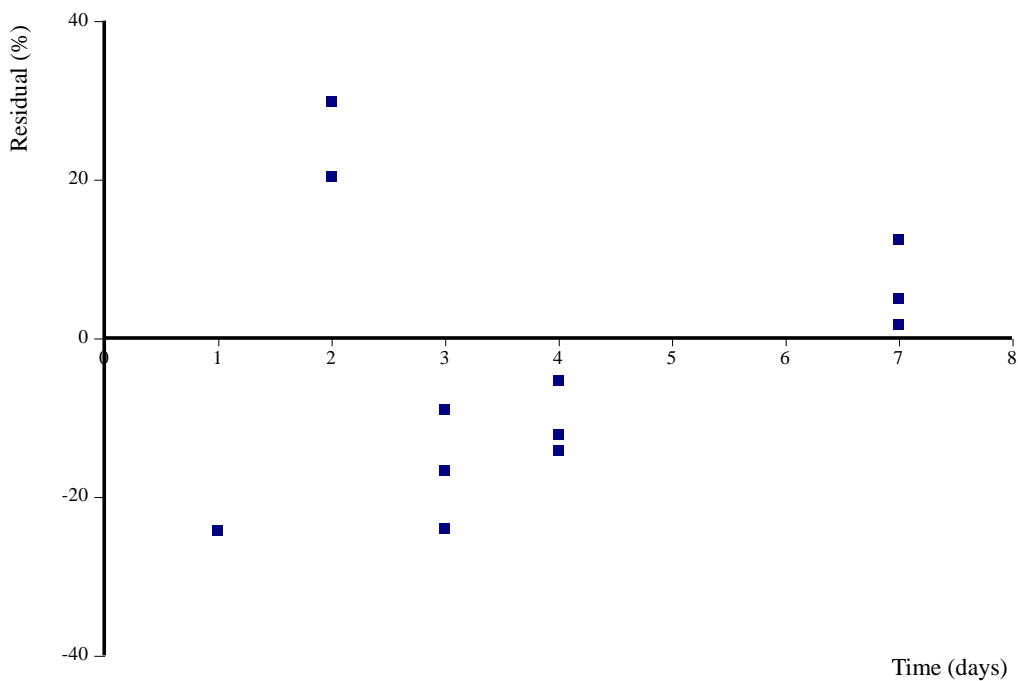
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

APPENDIX B**CAKE Kinetic Evaluation Report****Graphical Summary Nectar:****Observations and Fitted Model:**

DP Barcode: 447927

MRID No.: 50604601

Residuals:



Initial Values for this Step:

Parameter	Initial Value	Bounds	Fixed
Parent_0	100	0 to (unbounded)	No
k_Parent	0.1	0 to (unbounded)	No

Estimated Values:

Parameter	Value	σ	Prob. > t	Lower (90%) CI	Upper (90%) CI	Lower (95%) CI	Upper (95%) CI
Parent_0	219.9	53.47	N/A	123.9	315.9	102.2	337.6
k_Parent	0.5709	0.1226	3.49E-004	0.3507	0.7911	0.3011	0.841

χ^2

Parameter	Error %	Degrees of Freedom
All data	30.7	3
Parent	30.7	3

Decay Times:

Compartment	DT50 (days)	DT90 (days)
Parent	1.21	4.03

DP Barcode: 447927

MRID No.: 50604601

Additional Statistics:

Parameter	r ² (Obs v Pred)	Efficiency
All data	0.7803	0.7799
Parent	0.7803	0.7799

Parameter Correlation:

	Parent_0	k_Parent
Parent_0	1	0.9054
k_Parent	0.9054	1

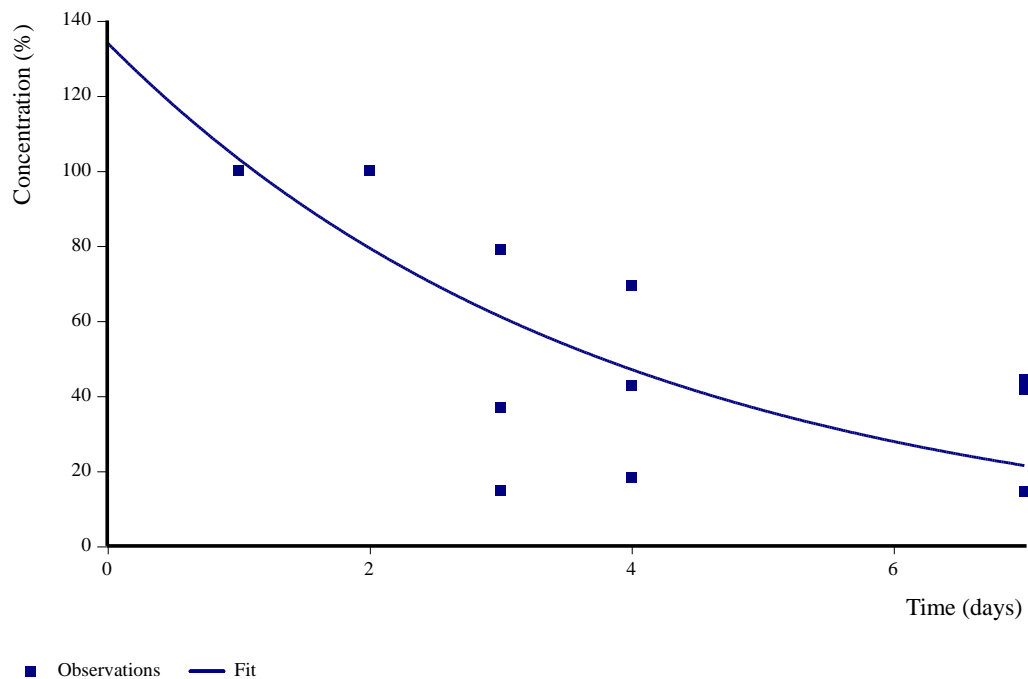
Observed v. Predicted:

Compartment Parent

Time (days)	Value (%)	Predicted Value	Residual
2	100	70.19	29.81
3	23	39.66	-16.66
4	17	22.41	-5.407
7	9	4.041	4.959
1	100	124.2	-24.24
2	90.6	70.19	20.41
3	15.6	39.66	-24.06
4	8.2	22.41	-14.21
7	16.5	4.041	12.46
2	100	70.19	29.81
3	30.7	39.66	-8.959
4	10.2	22.41	-12.21
7	5.7	4.041	1.659

Graphical Summary Pollen:

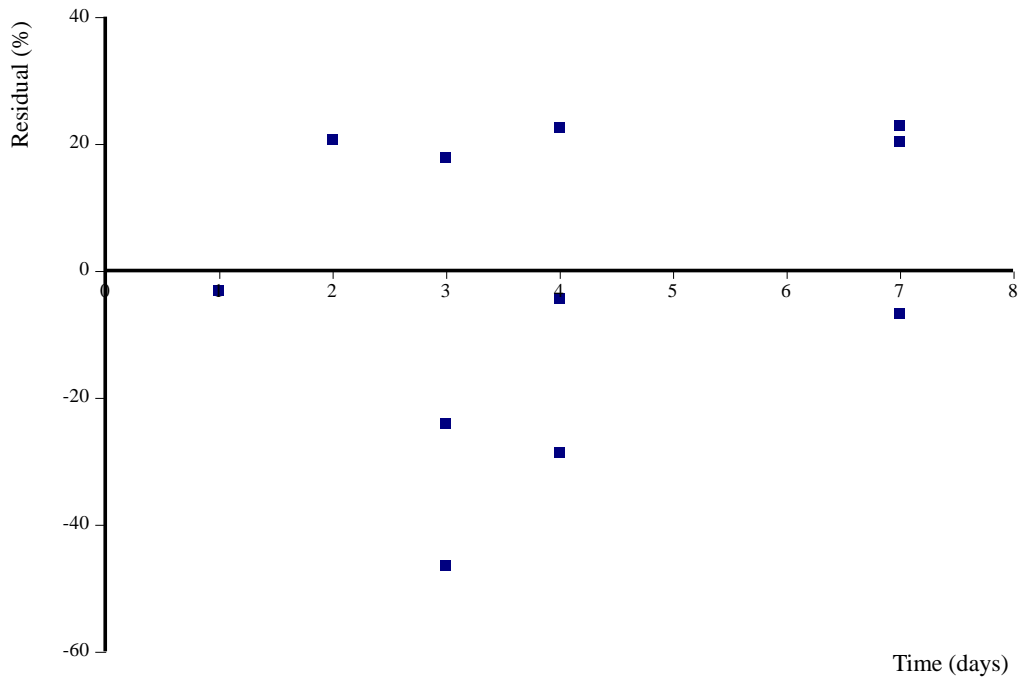
Observations and Fitted Model:



DP Barcode: 447927

MRID No.: 50604601

Residuals:



Initial Values for this Step:

Parameter	Initial Value	Bounds	Fixed
Parent_0	100	0 to (unbounded)	No
k_Parent	0.1	0 to (unbounded)	No

Estimated Values:

Parameter	Value	σ	Prob. > t	Lower (90%) CI	Upper (90%) CI	Lower (95%) CI	Upper (95%) CI
Parent_0	134.1	34.9	N/A	70.81	197.3	56.3	211.8
k_Parent	0.2619	0.09261	0.008956	0.09406	0.4298	0.05556	0.468

χ^2

Parameter	Error %	Degrees of Freedom
All data	16.8	3
Parent	16.8	3

Decay Times:

Compartment	DT50 (days)	DT90 (days)
Parent	2.65	8.79

DP Barcode: 447927

MRID No.: 50604601

Additional Statistics:

Parameter	r ² (Obs v Pred)	Efficiency
All data	0.4945	0.4897
Parent	0.4945	0.4897

Parameter Correlation:

	Parent_0	k_Parent
Parent_0	1	0.885
k_Parent	0.885	1

Observed v. Predicted:

Compartment Parent

Time (days)	Value (%)	Predicted Value	Residual
1	100	103.2	-3.182
3	78.9	61.11	17.79
4	69.5	47.03	22.47
7	44.3	21.44	22.87
2	100	79.41	20.59
3	37	61.11	-24.11
4	42.7	47.03	-4.329
7	41.7	21.44	20.27
2	100	79.41	20.59
3	14.7	61.11	-46.41
4	18.3	47.03	-28.73
7	14.6	21.44	-6.835

Sequence Creation Information:

Fit generated by CAKE version 3.3 (Release)
running on R version 3.0.0 (2013-04-03)

Report Information:

Report generated by CAKE version 3.3 (Release)
CAKE developed by Tessella Ltd, Abingdon, Oxfordshire, UK, sponsored by Syngenta
Running on .NET version 4.0.30319.42000